

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 10, 2006, 18:01:46 ; Search time 40.1584 Seconds

(without alignments)
1681.943 Million cell updates/sec

Title: US-10-734-564-72

Perfect score: 3721

Sequence: 1 MESPSAPHRWCIPWQRLL.....LSAGATGIMGVLVALLI 702

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3721	100.0	702	2	A36319
2	1609	43.2	526	1	A32164
3	1600.5	43.0	464	2	C30127
4	1589.5	42.7	417	2	JH0394
5	1470	39.5	286	2	A28333
6	1443	38.8	344	2	A27681
7	1427	38.3	351	2	JH0396
8	1423	38.2	321	2	JH0395
9	1272	34.2	349	2	A34815
10	1157.5	31.1	428	2	J50032
11	1148.5	30.9	419	2	JC4123
12	1141.5	30.7	428	2	I57486
13	1133.5	30.5	428	2	A27658
14	1130	30.4	436	2	B55181
15	1127.5	30.3	426	2	A35964
16	1127.5	30.3	426	2	S09016
17	1127.5	30.3	426	2	A35341
18	1127.5	30.3	495	2	A55181
19	1126.5	30.3	417	2	A28277
20	1126.5	30.3	419	2	A31135
21	1126.5	30.3	426	2	C55181
22	1126.5	30.3	426	2	B35334
23	1125.5	30.2	426	2	B33258
24	1124.5	30.2	419	2	A33258
25	1117.5	30.0	419	2	B54312
26	1107.5	29.8	435	2	D33258
27	1106.5	29.7	419	2	A36109
28	1099	29.5	424	2	A34595
29	1085.5	29.2	406	2	B43354

30	1080.5	29.0	395	2	D43354	pregnancy-specific
31	1078.5	29.0	397	2	C43354	pregnancy-specific
32	1070.5	28.8	521	2	S34338	biliary glycoprote
33	1069.5	28.7	458	2	JC1509	biliary glycoprote
34	1069	28.7	424	2	B36109	pregnancy-specific
35	1023.5	27.5	521	2	JC1508	biliary glycoprote
36	1018.5	27.4	458	1	MMMSR1	biliary glycoprote
37	988.5	26.6	519	2	A44783	ecto-ATPase precu
38	983	26.4	458	2	S68177	C-CAM2a protein is
39	965	25.9	458	2	S23969	cell-adhesion mole
40	919	24.7	402	2	A54312	pregnancy-specific
41	900.5	24.2	352	2	I77374	pregnancy-specific
42	898	24.1	332	2	JN0067	pregnancy-specific
43	892	24.0	335	2	H43354	pregnancy-specific
44	880	23.9	335	2	A33514	pregnancy-specific
45	889	23.9	326	2	JC4124	pregnancy-specific

ALIGNMENTS

RESULT 1
A36319
carcinoembryonic antigen precursor - human
N:Alternate names: CEA; meconium antigen 100
C:Species: Homo sapiens (man)
C:Date: 16-Sep-1992 #sequence revision 16-Sep-1992 #text change 09-Jul-2004
C:Accession: A36319; A27773; A31037; A25845; S08106; S31737; A44476; I54224; I59098; J
R:Schreier, H.; Thompson, J.; Bona, M.; Heftra, L.J.F.; Maruya, A.; Hasegawa, M.; Shive)
Mol. Cell. Biol. 10, 2738-2748, 1990
A:Title: Cloning of the complete gene for carcinoembryonic antigen: analysis of its p
A:Reference number: A36319; MUID:30258861; PMID:2342461
A:Accession: A36319
A:Molecule type: DNA
A:Residues: 1-702 <SCH>
A:Cross-references: UNIPROT:P06731; UNIPARC:UPI000003A84C; GB:M29540; NID:G180222; PIDN:AAA51967.1; F
A:Note: the authors show the codons TTA for residue 641-Phe and CAG for residue 646-T
R:Beauchemin, N.; Benchimol, S.; Cournoyer, D.; Fuks, A.; Stannere, C.P.
Mol. Cell. Biol. 7, 3221-3230, 1987
A:Title: Isolation and characterization of full-length functional cDNA clones for hum
A:Reference number: A27773; MUID:88038876; PMID:3670312
A:Accession: A27773
A:Molecule type: mRNA
A:Residues: 1-702 <BEA>
A:Cross-references: UNIPARC:UPI000003A84C; GB:M29540; NID:G180222; PIDN:AAA51967.1; F
A:Note: the authors translated the codon GNG for residue 130 as Leu
R:Oikawa, S.; Nakazato, H.; Kosaki, G
Biochem. Biophys. Res. Commun. 142, 511-518, 1987
A:Title: Primary structure of human carcinoembryonic antigen (CEA) deduced from cDNA
A:Reference number: A25845; MUID:87128144; PMID:3814146
A:Accession: A25845
A:Molecule type: mRNA
A:Residues: 5-702 <OIK>
A:Cross-references: UNIPARC:UPI000011DBE; GB:M15042; NID:G180198; PIDN:AAA51963.1; J
R:Oikawa, S.
submitted to the EMBL Data Library, September 1989
A:Reference number: S08106
A:Accession: S08106
A:Molecule type: mRNA
A:Residues: 5-319,321-702 <OIK>
A:Cross-references: UNIPARC:UPI000016A69F; EMBL:X16455; NID:G29854; PIDN:CAA34474.1; J
R:Barrett, T.
submitted to the EMBL Data Library, September 1991
A:Description: Genomic DNA sequence upstream of the translational start of the carc
A:Reference number: S31737

A:Accession: S31737
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-141 <BA2>
A:Cross-references: UNIPARC:UPI0000177089; EMBL:X62151
R:Khan, M.N.; Fraengsmeyer, L.; Teglund, S.; Israelsen, A.; Bremer, K.; Hammarstrom, S.
Genomics 14, 384-397, 1992
A>Title: Identification of three new genes and estimation of the size of the carcinoembryonic antigen
A:Reference number: A44476; MUID:93052339; PMID:1427854
A:Accession: A44476
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 35-141 <KHA>
A:Cross-references: UNIPARC:UPI000017708A
R:Willcocks, T.C.; Craig, I.W.
Genomics 8, 492-500, 1990
A>Title: Characterization of the genomic organization of human carcinoembryonic antigen
A:Reference number: 154224; MUID:91139118; PMID:2286372
A:Accession: 154224
A:Status: translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-37 <RES>
A:Cross-references: UNIPARC:UPI000016A69E; GB:M60964; MID:9180215; PIDN:AAA51972.1; PID:R:Siipen, D.; Paxton, R.J.; Neumaier, M.; Shively, J.E.; Wegener, C.
Biochem. Biophys. Res. Commun. 147, 212-218, 1987
A>Title: Carcinoembryonic antigen (CEA) and two crossreacting antigens of 165 KD and 105 KD
A:Reference number: A26831; MUID:87326349; PMID:3632664
A:Accession: A26831
A:Molecule type: protein
A:Residues: 35-64 <SIE>
A:Cross-references: UNIPARC:UPI000017708B
R:Thomas, P.; Toth, C.A.
Biochem. Biophys. Res. Commun. 170, 391-396, 1990
A>Title: Carcinoembryonic antigen binding to Kupffer cells is via a peptide located at the C-terminus
A:Reference number: A35490; MUID:90321257; PMID:2372297
A:Accession: A35490
A:Molecule type: protein
A:Residues: 'X', 140-151, 'X', 153, 'X', 155-156 <THO>
A:Cross-references: UNIPARC:UPI000017708C
A:Note: this is the amino terminal end of a fragment shown to mediate uptake by Kupffer cells
A:Comment: This is heavily glycosylated membrane protein of unknown function is a widely used C-terminus. This protein may be processed at its C-terminus. It is anchored to the membrane
C:Genes: CEA
A:Gene: GDB:CEA
A:Cross-references: GDB:119054; OMIM:114890
A:Map position: 19q13.2-19q13.2
A:Insertion: 22/1; 142/1; 235/1; 320/1; 413/1; 498/1; 591/1; 676/1
C:Superfamily: carcinoembryonic antigen, carcinoembryonic antigen precursor amino-terminal
C:Keywords: blocked carboxyl end, glycoprotein, lipoprotein, membrane protein, phosphatidylcholine, signal sequence, precursor amino-terminal homology <CEAN>
F:1-34/Domain: signal sequence #status predicted <SIG>
F:35-678/Product: carcinoembryonic antigen #status predicted <MAT>
F:160-217/Domain: immunoglobulin homology <IMM1>
F:252-301/Domain: immunoglobulin homology <IMM2>
F:338-395/Domain: immunoglobulin homology <IMM3>
F:516-573/Domain: immunoglobulin homology <IMM4>
F:608-657/Domain: immunoglobulin homology <IMM5>
F:678-702/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F:678/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Gly) (in mature form)

QY 1 NSSPAPRRKCI PMORLLLTSLTFMNPPTAKLTIESTPFNVASGKEVLLVHNLPQ 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 1 MESPAPRRKCI PMORLLLTSLTFMNPPTAKLTIESTPFNVASGKEVLLVHNLPQ 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 HLFQSWYSGEEVDGNRIIGVITGOATPGAVSGREIIPVASILLIONIIQNDIFY 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 61 HLFQSWYSGEVDGNRIIGVITGOATPGAVSREIIPVASILLIONIIQNDIFY 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 121 TLHAVIKSDLVNEBATQGFVYPPELPKPSISSNNSKPYEDKDVAFTCEPETODATYYLMWV 180
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 121 TLHAVIKSDLVNEBATQGFVYPPELPKPSISSNNSKPYEDKDVAFTCEPETODATYYLMWV 180
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 181 NNQSPLVSPRLQLSNCRNTLTLENTNRDPAKYKCEFQNVSAARSOSVILNLV YGPDPAP 240
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 181 NNQSPLVSPRLQLSNCRNTLTLENTNRDPAKYKCEFQNVSAARSOSVILNLV YGPDPAP 240
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 241 TISPLNTSVRSGENLNLSCHAAASNPPAOYSWFNGTFOQTGLEFIPIITVNSSGSYYCQ 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 241 TISPLNTSVRSGENLNLSCHAAASNPPAOYSWFNGTFOQTGLEFIPIITVNSSGSYYCQ 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 301 AANSDTGALNRRTVTYTIVYAEPKPETITSNNNSPVDEDAVALTCBEPIONTTYLMMVNN 360
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 301 AANSDTGALNRRTVTYTIVYAEPKPETITSNNNSPVDEDAVALTCBEPIONTTYLMMVNN 360
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 361 QGLPVSPRLQLSNDRNTLTLLSTRNDVGYEGCIONELSYDSHPYLNLV YGPDDPTI 420
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 361 QGLPVSPRLQLSNDRNTLTLLSTRNDVGYEGCIONELSYDSHPYLNLV YGPDDPTI 420
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 421 SPSTYYRGGVNLISLSCHAAASNPPAOYSWLIDGNIQHTGELFINSITEKNSSGLYTCQAN 480
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 421 SPSTYYRGGVNLISLSCHAAASNPPAOYSWLIDGNIQHTGELFINSITEKNSSGLYTCQAN 480
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 481 NSASGHSRITTVKTTIVYSAELPKPSISSNNSKPYEDKDVAFTCEPEAONTTYLMMVVNQSS 540
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 481 NSASGHSRITTVKTTIVYSAELPKPSISSNNSKPYEDKDVAFTCEPEAONTTYLMMVVNQSS 540
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 541 LPSVPRLOLSNGNRITLTENVTRNDARAIVCGIQNSISARSDPVTLDV YGPDTPITSP 600
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 541 LPSVPRLOLSNGNRITLTENVTRNDARAIVCGIQNSISARSDPVTLDV YGPDTPITSP 600
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 601 PSSSYSGANLNLSCHASASPPOYSWRINGIPQOHTQVFIAKITPPNNGTAYCFVSNL 660
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 601 PSSSYSGANLNLSCHASASPPOYSWRINGIPQOHTQVFIAKITPPNNGTAYCFVSNL 660
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 661 ATGRNNSIVKSITVSASGTS PGLSAGATVGIMIGVLGVALLI 702
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 661 ATGRNNSIVKSITVSASGTS PGLSAGATVGIMIGVLGVALLI 702
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
RESULT 2
A32164
biliary glycoprotein 1 precursor, splice form a - human
NlAlternat names: transmembrane carcinoembryonic antigen 1 (TM-CEA); transmembrane Ca.
NlContains: biliary glycoprotein 1, splice form b; biliary glycoprotein 1, splice form .
CjSpecies: Homo sapiens (man)
CjDate: 20-Apr-2000 #sequence revision 20-Apr-2000 #text change 09-Jul-2004
CjAccession: A32164, A30127, B30127, A48078, S45664, S65939, A30847, G44476
R.Hinda. Y.; Neumaler, M.; Hefta, S.A.; Drexler, Z.; Wagener, C.; Shively, L.; Hefta,
Proc. Natl. Acad. Sci. U.S.A. 86, 1668, 1989
AjReference number: A32164
AjContents: extraum
AjAccession: A32164
A.Molecule type: mRNA
A.Residues: 1-526 <HIN>
A.Cross-references: UNIPROT:P13688; UNIPARC:UPI0000127483; GB:J03858, NTD:g179439, PIDN
R.Hinda. Y.; Neumaler, M.; Hefta, S.A.; Drexler, Z.; Wagener, C.; Shively, L.; Hefta,
Proc. Natl. Acad. Sci. U.S.A. 85, 6959-6963, 1988
AjTitle: Molecular cloning of a cDNA coding biliary glycoprotein I : Primary structure of
A.Reference number: A94206, PMID:8832055; PMID:2457922
AjContents: annotation
AjNote: The sequence shown in this reference has been completely corrected in reference
J.Barrett, T.R.; Kretschmer, A.; Austen, D.A.; Goebel, S.J.; Hart, J.T.; Elting, J.J., F
J. Cell Biol. 108, 267-276, 1989

Query Match 43.2%; Score 1609; DB 1; Length 526;
Best Local Similarity 62.7%; Pred. No. 3.7e-80;
Matches 326; Conservative 47; Mismatches 121; Indels 26; Gaps 6;

5 SAPPHRWICIPWQALLTASLITFNPTTKALTIESTPFPNVAEGKEVLLVHNLDOHLFG 64

Query Match 43.0%; Score 1600.5; DB 2; Length 464;
Best Local Similarity 73.0%; Pred. No. 9.1e-80;
Matches 309; Conservative 30; Mismatches 79; Indels 5; Gaps 2;

[illegible]

```

Db      125  I KSLVNHBEATGCFHHYPPELPKPSISNNNSNPVEDCDAAVFCPEPTQDTTILMTNNOS 184
QY      185  LPVSPRLQSLNSGRRTLLFNVTNRNDTPASYKCETONPVASRRSDVTILNVLYGDAFTISP 244
Db      185  LPVSPRLQSLNSGRRTLLFNVTNRNDTPAYECEIQNVSNANRSDPVTILNTYGDPTTISP 244
QY      245  LMTSYRSGEMLNLSCHASNPQAQYMPVNGTFOGQSTOELFPINTIVNNSSGYTCAHNS 304
Db      245  SDTYIRRGANLISLSCVAASNPPAQYEWLNGTFOGQSTOELFPINTIVNNSSGYTCAHNS 304
QY      305  DTGNLRRTVTTTITYAEP---KPFTSSNNSVEVEDDAVLTCEPEIQNTTYLWVNNQ 361
Db      305  VTGNCRRTVTTTIVTSLSPVAKPQIKASTVTYTGKDSVNLTCSTNDTGISIRWFEPKQ 364
QY      362  SLPPSPRLQSLNSNRRTLLTSLVTRNDVGPYECGQIQNELSVDSHDPYILNV 411
Db      365  SLPSSERMKLISQGNITTLISNPVAREDDAGTYWCVFNPISKQSDPITMLNV 414

RESULT 5
A28333
carcinoembryonic antigen-related protein (clone eLv7) - human (fragment)
C1Species: Homo sapiens (man)
C1Date: 19-May-1989 #sequence_revision 19-May-1989 #ext_change 09-Jul-2004
C1Accession: A28333
R1Kmarck, M.E.; Elting, J.J.; Hart, J.T.; Goebel, S.J.; Rae, P.M.M.; Nothdurft, M.A
Article: Carcinoembryonic antigen family: expression in a mouse L-cell transfectant at
A1Reference number: A28333; MUID:87260984; PMID:2955415
A1Accession: A28333
A1Molecule type: mRNA
A1Residues: 1-286 <KAM>

```

```

RESULT 4
JH0394
Biliary glycoprotein g precursor - human
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C/Accession: JH0394
R/Kuruki, M.; Arakawa, F.; Matsuo, Y.; Oikawa, S.; Nakazato, H.; Matsuka, Y.
Biochem. Biophys. Res. Commun. 176, 578-585, 1991
A/Title: Three novel molecular forms of biliary glycoprotein deduced from cDNA clones fr
A/Reference number: JH0394; MUID:9122218; PMID:2025273
A/Accession: JH0394
A/Molecule type: mRNA
A/Residues: 1-417 <KIR>
A/Cross-references: UNIPROT:P13688; UNIPARC:UPI000002A624; GB:M72238; NID:G179436; PIDN:
A/Experimental source: leukocyte
C/Comment: Biliary glycoproteins belong to the carcinoembryonic antigen gene family.
C/Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termi
C/Keywords: glycoprotein; transmembrane protein
F.1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F.1-34/Domain: signal sequence #status predicted <SIG>
F.35-383/Product: biliary glycoprotein g #status predicted <MAT>
F.160-217/Domain: immunoglobulin homology <IMM1>
F.252-301/Domain: immunoglobulin homology <IMM2>
F.341-398/Domain: immunoglobulin homology <IMM3>

Query Match 42.7%; Score 1589.5; DB 2; Length 417;
Best Local Similarity 74.4%; Pred. No. 3.le-79;
Matches 305; Conservative 28; Mismatches 74; Indels 3; Gaps 1;

OY 5 SAPPHRCIIPQORLLTASTLTFNNPPTAKLTIESPPENVAEKEVILLVHNIPQHLFG 64
SAPHHRCIIPQORLLTASTLTFNNPPTAKLTIESPPENVAEKEVILLVHNIPQHLFG 64
Db 5 SAPLHRARVPMQGLLTSLTFNNPPTAQLTIESMPEFNVAEGEVLVHNIPQHLFG 64
SAPLHRARVPMQGLLTSLTFNNPPTAQLTIESMPEFNVAEGEVLVHNIPQHLFG 64

OY 65 YSMYKGEKRVNDROILIGVIGTQDTPGPAASGREIIPNASTLIONIQNDTGYTLAH 124
YSMYKGEKRVNDROILIGVIGTQDTPGPAASGREIIPNASTLIONIQNDTGYTLAH 124
Db 65 YSMYKGEKRVNDROILIGVIGTQDTPGPAASGREIIPNASTLIONIQNDTGYTLQV 124
YSMYKGEKRVNDROILIGVIGTQDTPGPAASGREIIPNASTLIONIQNDTGYTLQV 124

OY 125 IKSLDVLNEATGQFRVRYPELPEKPSISSNNKSPVEDKQAVATCEPEFDATYLLMWNQOS 184
IKSLDVLNEATGQFRVRYPELPEKPSISSNNKSPVEDKQAVATCEPEFDATYLLMWNQOS 184

```

Query Match		39.5%; Score 1470; DB 2; Length 286;
Best Local Similarity		98.6%; Pred. No. 5.8e-73;
Matches	276; Conservative	2; Mismatches 2; Indels 0; Gaps 0;
F/23-80/Domain: immunoglobulin homology <IMM1>		
F/115-164/Domain: immunoglobulin homology <IMM2>		
F/201-258/Domain: immunoglobulin homology <IMM3>		
QY	322	PPKPPITSNNSNPVEDEDAVALTCEPIQNTTYLMMVNNQSLPVSPRLQLSNDRTLTLL 381
DB	7	PIKPFITSNNSNPVEDEDAVALTCEPIQNTTYLMMVNNQSLPVSPRLQLSNDRTLTLL 66
QY	382	SVTENDVGPVCGIQNELSDVSHDPVLTANLVGYPDDPTISPYTYYPGVNLISCHAA 441
DB	67	SVTENDVGPVCGIQNELSDVSHDPVLTANLVGYPDDPTISPYTYYPGVNLISCHAA 126
QY	442	NPAPQYSLIDGNIQCHTOELFISNTERKNSGLTCCANNASAGSHRTYKTTIVSALP 501
DB	127	NPAPQYSLIDGNIQCHTOELFISNTERKNSGLTCCANNASAGSHRTYKTTIVSADV 186
QY	502	KPSSISNNKSPVEDKDAVAFTCEPEAQNTTYLMMVNGQSLPVSPRLQLSNGRTLTLLFN 561
DB	187	KPSSISNNKSPVEDKDAVAFTCEPEAQNTTYLMMVNGQSLPVSPRLQLSNGRTLTLLFN 246
QY	562	TRNDARAYVCIGIONSVSANRSDPYTLDVLYGPDPTIISP 601
DB	247	TRNDARAYVCIGIONSVSANRSDPYTLDVLYGPDPTIISP 286
RESULT 6		
A27681		
nonspecific cross-reacting antigen precursor - human		
N.Alternate names: NCA; TEX/NCA		
C.Species: Homo sapiens (man)		
C.Date: 31-Mar-1989 #sequence revision 16-Sep-1992 #text change 09-Jul-2004		
C.Accession: A26902; A29875; A27681; B31037; A29818; A27709; A36271; C26414; E44476; F44476		
R.Oikawa, S.; Kosaki, G.; Nakazato, H.		
Biochem. Biophys. Res. Commun. 146, 464-469, 1987		
AltTitle: Molecular cloning of a gene for a member of carcinoembryonic antigen (CEA) gene		

A:Reference number: A26902; MUID:87298464; PMID:3619891
 A:Accession: A26902
 A:Molecule type: DNA
 A:Residues: 1-141 <OK>
 A:Cross-references: UNIPROT:Q13774; UNIPARC:UPI0000072416; GB:M17082; NID:g180230; PIDN:R1Thompson, J.A.; Pande, H.; Paxton, R.J.; Shively, L.; Padma, A.; Slimmer, R.L.; Todd, C
 Proc. Natl. Acad. Sci. U.S.A. 84, 2965-2969, 1987
 A:Title: Molecular cloning of a gene belonging to the carcinoembryonic antigen gene family
 A:Reference number: A29875; MUID:87204248; PMID:3033672
 A:Accession: A29875
 A:Molecule type: DNA
 A:Residues: 23-141 <THO>
 A:Cross-references: UNIPARC:UPI0000177070; GB:M16337
 A:Note: the authors translated the codon ACT for residue 64 as Tyr
 R:Tsawagi, Y.; Okawa, S.; Matsuo, Y.; Kosaki, G.; Nakazato, H.
 Biochem. Biophys. Res. Commun. 150, 89-96, 1988
 A:Title: Primary structure of non-specific cross-reacting antigen (NCA), a member of carcinoembryonic antigen family
 A:Reference number: A27681; MUID:88106638; PMID:3337731
 A:Accession: A27681
 A:Molecule type: mRNA
 A:Residues: 1-238 'V', 240-344 <TAM>
 A:Cross-references: UNIPARC:UPI000012748C; GB:M18728; NID:g189084; PIDN:AAA59907.1; PID:R:Barneit, T.; Goebel, S.O.; Notchduft, M.A.; Elting, J.C.
 Genomics 3, 59-66, 1988
 A:Title: Carcinoembryonic antigen family: characterization of cDNAs coding for NCA and C
 A:Reference number: A31037; MUID:89122014; PMID:3220478
 A:Accession: B31037
 A:Molecule type: mRNA
 A:Residues: 1-137, 'L', 139-344 <BAR>
 A:Cross-references: UNIPARC:UPI000016AD06; GB:M29541; NID:g189103; PIDN:AAA59915.1; PID:R:Neumeier, M.; Zimmermann, W.; Shively, L.; Hinda, Y.; Riggs, A.D.; Shively, J.E.
 J. Biol. Chem. 263, 3202-3207, 1988
 A:Title: Characterization of a cDNA clone for the non-specific cross-reacting antigen (NCA)
 A:Reference number: A29918; MUID:88139389; PMID:2830274
 A:Accession: A29918
 A:Molecule type: mRNA
 A:Residues: 1-344 <NEU>
 A:Cross-references: UNIPARC:UPI000006D42; GB:M18216; GB:J03550; NID:g178690; PIDN:AAA51
 R:Grunert, F.; Kolbinger, F.; Schwarz, K.; Schwabold, H.; von Klitzsch, S.
 Biochem. Biophys. Res. Commun. 153, 1105-1115, 1988
 A:Title: Protein analysis of NCA-50 shows identity to NCA cDNA deduced sequences and ind
 A:Reference number: A27709; MUID:88268882; PMID:3390172
 A:Accession: A27709
 A:Molecule type: protein
 A:Residues: 35-95; 99-120; 123-138; 149-151, 'X', 153-162; 166, 'X', 168-172, 'X', 174-193; 221-235
 A:Cross-references: UNIPARC:UPI0000177071; UNIPARC:UPI0000177072; UNIPARC:UPI0000177073;
 078; UNIPARC:UPI0000177079; UNIPARC:UPI0000177074
 R:Hefta, S.A.; Paxton, R.J.; Shively, J.E.
 J. Biol. Chem. 265, 8618-8626, 1990
 A:Title: Sequence and glycosylation site identity of two distinct glycoforms of nonspect
 A:Reference number: A26271; MUID:90256782; PMID:2341397
 A:Accession: A26271
 A:Molecule type: protein
 A:Residues: 35-42; 44-53; 55-80; 83-114; 139-160; 166-172; 174-180; 191-194; 204-224; 233-308; 310
 A:Cross-references: UNIPARC:UPI0000177078; UNIPARC:UPI0000177079; UNIPARC:UPI000017707C; UNIPARC:UPI000017707D;
 082; UNIPARC:UPI0000177083; UNIPARC:UPI0000177084
 R:Paxton, R.J.; Mosser, G.; Pande, H.; Lee, T.D.; Shively, J.E.
 Proc. Natl. Acad. Sci. U.S.A. 84, 920-924, 1987
 A:Title: Sequence analysis of carcinoembryonic antigen: identification of glycosylation
 A:Reference number: A26414; MUID:87147209; PMID:3469550
 A:Accession: C26414
 A:Molecule type: protein
 A:Residues: 35-69 <PAX>
 A:Cross-references: UNIPARC:UPI0000177085
 R:Khan, W.N.; Fraenkel, L.; Teglund, S.; Israelsson, A.; Bremer, K.; Hammarstrom, S.
 Genomics 14, 384-390, 1992
 A:Title: Identification of three new genes and estimation of the size of the carcinoemb
 A:Reference number: A4476; MUID:93052339; PMID:1427854
 A:Accession: B4476
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 35-141 <KHA>

A:Cross-references: UNIPARC:UPI0000177086
 A:Accession: F4476
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 35-137 'L', 139-141 <KH2>
 A:Cross-references: UNIPARC:UPI0000177086
 C:Comment: This protein appears to be processed at the carboxyl terminus and anchored
 C:Gene: GDB:NCA
 A:Cross-references: GDB:120221; OMIM:163980
 A:Map position: 19q13.2-19q13.2
 A:Introns: 22/1
 A:Note: the list of introns may be incomplete
 C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-ter
 C:Keywords: blocked carboxyl end; glycoprotein; lipoprotein; membrane protein; phosph
 F:1-138/Domain: signal sequence #status predicted <SIG>
 F:139-344/Domain: signal sequence #status predicted <SIG>
 F:35-320/Product: nonspecific cross-reacting antigen #status experimental <MAT>
 F:160-217/Domain: immunoglobulin homology <IMM1>
 F:252-301/Domain: immunoglobulin homology <IMM2>
 F:321-344/Domain: carboxyl-terminal propeptide #status predicted <CTP>
 F:104,111,115,152,173,197,224,256,274,288,292/Binding site: carbohydrate (Asn) (coval
 F:309/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:320/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Gly) (in mature f
 Query Match 38.8%; Score 1443; DB 2; Length 344;
 Best Local Similarity 83.9%; Pred. No. 2,1e-71;
 Matches 271; Conservative 11; Mismatches 41; Indels 0; Gaps 0;
 QY 1 MESPSAPPRHRCIPWQRLTLTASLTFTFNPPTAKLTITESTPNNVAGKEVLLVHNLPO 60
 DB 1 MGPSPAPPCRLHVPKVEVLLTSLTFTFNPPTAKLTITESTPNNVAGKEVLLVHNLPO 60
 QY 61 HLFSGYKGERVDGNQRIIGYVIGTQATPGPAGSGRETIYNNASLLIGNIIONDTGFY 120
 DB 61 NRGYSWYKGERVDGNLSLVGVYIGTQATPGPAGSGRETIYNNASLLIGNIIONDTGFY 120
 QY 121 TLHVTKSDLVNBEATQGFERYPELPKPSISSNNKVEVDKDAVFCPEPTQATYLMW 180
 DB 121 TLQVTKSDLVNBEATQGFERYPELPKPSISSNNKVEVDKDAVFCPEPTQATYLMW 180
 QY 181 NNQSLPVSRLQSLNENRITLTFTFNTRNTASFKCTONPVSARSDSVLYLVGPDAP 240
 DB 181 NGQSLPVSRLQSLNENRITLTFTFNTRNTASFKCTONPVSARSDSVLYLVGPDAP 240
 QY 241 TISPLNTSYRSGENLNLSCAASNPAPQYSWFGNFTQOSTQELFIPNITVNNSGSYTCQ 300
 DB 241 TISPSKANRPRPENLNLSCAASNPAPQYSWFGNFTQOSTQELFIPNITVNNSGSYTCQ 300
 QY 301 AHNSTGLNRTTITVTVYAPBP 323
 DB 301 AHNSTGLNRTTITVTVYAPBP 323
 RESULT 7
 JH0396
 biliary glycoprotein i precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
 A:Accession: JH0396
 R:Kuraki, M.; Arakawa, F.; Matsuo, Y.; Oikawa, S.; Nakazato, H.; Matsuo, Y.
 Biochem. Biophys. Res. Commun. 176, 578-585, 1991
 A:Title: Three novel molecular forms of biliary glycoprotein deduced from cDNA clone
 A:Reference number: JH0394; MUID:91222218; PMID:2025273
 A:Accession: JH0396
 A:Molecule type: mRNA
 A:Residues: 1-351 <KUR>
 A:Cross-references: UNIPROT:P13688; UNIPARC:UPI000002A626; GB:M72238; NID:g179436; I
 A:Experimental source: leukocyte
 C:Comment: Biliary glycoproteins belong to the carcinoembryonic antigen gene family
 C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-ter
 C:Keywords: glycoprotein; transmembrane protein
 F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>

F_1-34/Domains: signal sequence #status predicted <SIS>
F_35-351/Product: biliary glycoprotein 1 #status predicted <MAT>
F_160-217/Domains: immunoglobulin homology <IM1>
F_252-301/Domains: immunoglobulin homology <IM2>

Query Match	38.3%;	Score 1427;	DB 2;	length 351;
Best Local Similarity	84.6%;	Pred. No. 1.6e-70;		
Matches 269;	Conservative 12;	Mismatches 37;	Indels 0;	Gaps 0;

OY	5	SAPHRWCIPQORLLITLITFEMNPPTAKLTIESTPEVNAEKKVLLVHNLPHQLFC	64
Db	5	SAPHRVNRVPWQGLLITLITFNPPTTRQOLTTEMPFNVAEKKVLLVHNLPHQLFC	64
OY	65	YSWYGERVDGNROIIIGYITGOATPGAYSRELIYPNLSLIIIONIDTGFPTLHV	124
Db	65	YSWYGERVDGNROIVGVAIGTOAAPGANSGRELIYPNLSLIIIONVDNDGYFTLOV	124
OY	125	IKSDLVNEEATGQFRYPYLPKPSISSNKS.PVEDDQDAVAFTCEPEFODATYLMWNOS	184
Db	125	IKSDLVNEEATQGFHYLPKPSISSNKS.NPVEDDQDAVAFTEPEFODTTIYLMWINOS	184
OY	185	LPVSPRLQISNGRITLTENVTRNDTPASIKCETONPVASARSDSVLLNLYGEDAPTIS	244
Db	185	LPVSPRLQISNGRITLTLSVRNDTPGYPECEIQNPSANRSDPVLNLYGGDPTIIS	244
OY	245	INTSYRSGENLNISCHAAENP.PAOYSMPFNGTFOQSTOELEFINITVNNSGSYCOAHNS	304
Db	245	SPTYYRPGANLSLSCAASN.PPAQYSMLNGTFOQSTOELEFINITVNNSGSYTCHAHNS	304
OY	305	DTGLNRITVTTIITVYAP	322
Db	305	VTGCNRTIVKIIIVTESP	322

RESULT 8
JH0395
biliary glycoprotein h precursor - human
C|Species: Homo sapiens (man)
C|Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C|Accession: JH0395
R|Kutokki, M.; Arakawa, F.; Matsuo, Y.; Oikawa, S.; Nakazato, H.; Matsuo, Y.
Biochem. Biophys. Res. Commun. 176, 578-585, 1991
A|Title: Three novel molecular forms of biliary glycoprotein deduced from cDNA clones
A|Reference number: JH0394; MUID:91222218; PMID:2025273
A|Accession: JH0395
A|Molecule type: mRNA
A|Residues: 1-321 <KID>
A|Cross-references: UNIPROT:P13688; UNIPARC:UP000002A2625; GB:M69176; NID:G179434; PIDN:
A|Cross-references: UNIPROT:leukocyte
A|Experimental source: leukocyte
C|Comment: Biliary glycoproteins belong to the carcinoembryonic antigen gene family.
C|Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termi
C|Keywords: glycoprotein; transmembrane protein
F1-138/Domin: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F1-34/Domin: signal sequence #status predicted <SIG>
F135-321/Product: biliary glycoprotein h #status predicted <MAT>
F160-217/Domin: immunoglobulin homology <IMM1>
F1252-301/Domin: immunoglobulin homology <IMM2>

Query Match	Similarity	Score	DB 2;	Length	321;
Best Local	85.4%	Pred.	No. 2,4e-70;		
Matches	268;	Conservative	12;	Mismatches	34;
				Indels	0;
				Gaps	0
QY	5	SAPPRMCTPWRLLTASLTTPWNPPTAKLTIESPPNVAEGKEVLLVHNLPOHLFG	64		
DB	5	SAPLHRVRVPWGGLLTASLTTPWNPPTTQLTTPSPFNVAEGKEVLLVHNLPOOLF	64		
QY	65	YSMYGERVDGNKROLIGYVIGTQATPPGPAVSGREIYPNASSLLIQNIIONDGFYTLAV	124		
DB	65	YSMYGERVDGNKROLIGYVIGTQATPPGPAVSGREIYPNASSLLIQNVQNDGFGYTLQV	124		
QY	125	IKSDLVNEEATGQFRVYPPELPKPSISSNNKSPVEDKDAVAFCEPFTODATYLMVNNQS	184		
DB	125	IKSDLVNEEATGQFHYVPELPKPSISSNNKSPVEDKDAVAFCEPFTODTYYLMVNNQS	184		

[illegible]

RESULT 9

A34815

carcinoembryonic antigen family member CGM6 precursor - human

N/Alternate names: carcinoembryonic antigen family member NCA-95; CD67; nonspecific c.

C/Species: Homo sapiens (man)

C/Date: 13-Jul-1990 #sequence revision 02-Aug-1996 #text_change 09-Jul-2004

C/Accession: S13524; I44476; A34815

R/Berling, B.; Kolbinger, F.; Gurnert, F.; Thompson, J.A.; Brombacher, F.; Buchegger, Cancer Res. 50: 6534-6539, 1990

A/Title: Cloning of a carcinoembryonic antigen gene family member expressed in leukocy

A/Reference number: S13524; MUID:91003998; PMID:2208113

A/Accession: S13524

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-349 <BER>

A/Cross-references: UNIPROT:P31997; UNIPARC:UPI000016A6BD; EMBL:X52378; NID:G29918; PI R/Khan, W.N.; Fraengemyr, L.; Teglund, S.; Israelsson, A.; Bremer, K.; Hammarstrom, S Genomics 14: 384-390, 1992

A/Title: Identification of three new genes and estimation of the size of the carcinoem

A/Reference number: A4476; MUID:93052339; PMID:1427854

A/Accession: I4476

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: DNA

A/Residues: 35-141 <KHA>

A/Cross-references: UNIPARC:UPI00001770BD

R/Aikawa, F.; Kuroki, M.; Matsui, Y.; Okawa, S.; Nakazato, H.; Matsumoto, Y. Biochem. Biophys. Res. Commun. 166: 1063-1071, 1990

A/Title: Characterization of a cDNA clone encoding a new species of the nonspecific cr

A/Reference number: A34815; MUID:90165902; PMID:2306228

A/Accession: A34815

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-113, 'R', '115-321, 'V', '223-349 <ARA>

A/Cross-references: UNIPARC:UPI000016A6C5; GB:ID90064; NID:G219935; PTDN:BA14108.1; PTD

A/Experimental source: white blood cells

C/Genetics:

A/Gene: GDB:CGM6

A/Cross-references: GDB:127667

A/Map position: 19q13.2-19q13.2

C/Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termi

C/Keywords: phosphatidylinositol linkage

F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>

F:160-217/Domain: immunoglobulin homology <IMM1>

F:252-301/Domain: immunoglobulin homology <IMM2>

Query Match	34.2%	Score 1272;	DB 2;	Length 349;
Best Local Similarity	76.8%;	Pred. No. 4.1e-62;		
Matches 241; Conservative	19;	Mismatches 54;	Indels 0;	Gaps 0

QY	5	SAPHRWCIPQORLLITLNSLFTFNNPPTAKLTISTEPNNAEGKEVLLVHNLPOHLFG	64
DB	5	SAPSCRWRHPIQOGILLTSLFTFNNPPTAQITITAVPSNAEGKEVLLVHNLPODPRG	64
QY	65	YSWYKGERVDGNRQITIGVICTQATPCGPAYSGREIITPMASLLIQNIQNDTGFTLHV	124
DB	65	YNNWYGERVTDNRRIIGVIVISNQITTPGPAYSNRETIIPNASLLMRNVTAKNDTGSYTLQV	124
QY	125	IKSLDVLNEEATGQFRVYVPELPEKPSITSSNNKSPVEDKDAVFTCEPETODATYLLMWVNNOS	184

Db 125 IKLNLMSSEVTSQFVSHPETPKPSISSNNSNPVEDKDAVAFTCEPETONTTTLMTWNGOS 184
 QY 185 LPVSPRLQSLNSGRNTLTLLFNVTNRNDPTASKYCETONPVASRSDSVLTNLVYGDPAFTISP 244
 Db 185 LPVSPRLQSLNSGRNTLTLLFNVTNRNDPTASKYCETONPVASRSDSVLTNLVYGDPAFTISP 244
 QY 245 LNTSYRSGENLNLSCHAASNPAPQYSWFWNGTFOQSTOELFIPNITVNNSGSYTCQAHNS 304
 Db 245 SDTYHAGVNLNLSCHAASNPQYSWSVNGTFOQTOKLFIPIITTKNSGSYACHTTMS 304
 QY 305 DTGLNRTTYYTITV 318
 Db 305 ATGRNRTTYRMATV 318

RESULT 10
 JS0032
 pregnancy-specific beta-1 glycoprotein 3 precursor - human
 N:Alternate names: pregnancy-specific beta-1 glycoprotein A precursor
 C:Species: Homo sapiens (man)
 C>Date: 31-Mar-1992 #sequence revision 31-Mar-1992 #text change 09-Jul-2004
 C:Accession: JS0032; F03038; A32719; C35341; B34647; A35334
 R:Rooney, B.C.; Horne, C.H.W.; Hardman, N.
 Gene 71, 439-449, 1988
 A:Title: Molecular cloning of a cDNA for human pregnancy-specific beta 1-glycoprotein: H
 A:Reference number: JS0032; MUID:89138020; PMID:3265688
 A:Accession: JS0032
 A:Molecule type: mRNA
 A:Residues: 1-428 <R00>
 A:Cross-references: UNIPROT:Q16557; UNIPARC:UPI000002D1C2; GB:M23575; NID:g183596; PIDN:
 A:Accession: P50308
 A:Molecule type: protein
 A:Residues: 50-69,99-113,160-167,210-216,266-275,337-344 <R02>
 A:Cross-references: UNIPARC:UPI00001770A1; UNIPARC:UPI00001770A2; UNIPARC:UPI00001770A3;
 R:Steydlo, C.; Swillens, S.; Georges, M.; Szpiter, C.; Vaseart, G.
 Genomics 6, 579-592, 1990
 A:Title: Structure, evolution and chromosomal localization of the human pregnancy-specif
 A:Reference number: A32719; MUID:90256167; PMID:2341148
 A:Accession: A32719
 A:Molecule type: mRNA
 A:Residues: 1-428 <STR>
 A:Cross-references: UNIPARC:UPI000002D1C2; GB:M34420; NID:g183594; PIDN:AAA52606.1; PID:
 R:Zoubir, F.; Khan, W.N.; Hammarstrom, S.
 Biochem. Biophys. Res. Commun. 169, 203-216, 1990
 A:Title: Carcinoembryonic antigen gene family members in submandibular salivary gland: c
 A:Reference number: A35341; MUID:90274668; PMID:2350345
 A:Accession: C35341
 A:Molecule type: mRNA
 A:Residues: 1-428 <ZOU>
 A:Cross-references: UNIPARC:UPI000002D1C2; GB:M37399; NID:g180234; PIDN:AAA60958.1; PID:
 R:Botjagin, J.; Teese, L.A.; Barnes, W.; Chan, W.Y.
 Biochem. Biophys. Res. Commun. 166, 622-629, 1990
 A:Title: Expression of the pregnancy-specific beta 1-glycoprotein genes in human testis.
 A:Reference number: A34647; MUID:90147764; PMID:2302228
 A:Accession: B34647
 A:Molecule type: mRNA
 A:Residues: 23-329,384-428 <BOR>
 A:Cross-references: UNIPARC:UPI00001770A7; UNIPARC:UPI00001770A8
 A:Note: the mRNA sequenced here has both a deletion and an unspliced intron
 C:Comment: This protein plays an essential role in normal pregnancy. It is a well-charac
 elis.
 C:Genetics:
 A:Gene: GDB:PSG3
 A:Cross-references: GDB:128239; OMIM:176392
 A:Map position: 19q13.2-19q13.2
 C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termi
 C:Keywords: glycoprotein; membrane protein; carcinoembryonic antigen precursor amino-termi
 F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
 F:1-14/Domain: signal sequence #status predicted <SIG>
 F:35-428/Product: pregnancy-specific beta-1-glycoprotein #status predicted <MAT>
 F:162-219/Domain: immunoglobulin homology <IMM1>
 F:255-312/Domain: immunoglobulin homology <IMM2>

F:247-396/Domain: immunoglobulin homology <IMM3>
 F:104,111,268,303/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 31.1%; Score 1157.5; DB 2; Length 428;
 Best Local Similarity 47.8%; Pred. No. 8,7e-56;
 Matches 237; Conservative 51; Mismatches 121; Indels 87; Gaps 3;

QY 5 SAPRHWCIPMORLLTASTLTFWNPPTAKLTISTEPNVAEGKVLVLLVHNLPOHLPG 64
 Db 5 SAPRQRTTWKGLTLASLNLNFMNPPTAAQTIEAPTKVSAGKQVLLVHNLVPLNLAG 64
 QY 65 YMYKGERVDGNROIIGVYGTQATPGPAYGREIIVNPNASLLIIONDGFYTLHV 124
 Db 65 YIMYQGMKMDLVHYITSYVDGQIIHYGPAISGREIVYNASLLIONVREDGSTLHI 124
 QY 125 IKSDLVNEATGQ--FRVYPELPKPSISSNNSKPVEDKDAVAFTCEPETODATYTLWVN 182
 Db 125 VKRGDTRGRTGFTFTLYLETPEKPSISSNLYPEDEMAVASLTCDEPTPDASYLWVNG 184
 QY 183 QSLPVSRLQSLNSGRNTLTLLFNVTNRNDPTASKYCETONPVASRSDSVLTNLVYGDPAFTI 242
 Db 185 QSLPMTSHLSQSLNSGRNTLFLFVTKYTAGPYCELRNPVSARSDEVTNLNL----- 236
 QY 243 SPLNTSYRSGENLNLSCHAASNPAPQYSWFWNGTFOQSTOELFIPNITVNNSGSYTCQAH 302
 Db 237 -----PKL----- 239
 QY 303 NSDTGLNRTTYYTITVYAPPKPFITSSNNSNPVEDKDAVALTCEPEIONTTTLMTWNGOS 362
 Db 240 -----PKPYITINLNPRENDVLAFTCEPESENYTYIMWNGOS 279
 QY 363 LPVSPRLQSLNSGRNTLTLLFNVTNRNDPTASKYCETONPVASRSDSVLTNLVYGDPAFTISP 422
 Db 280 LPVSPRVKRPINRLILIPSVTRNEGPOCEIQRGGIRSYPTVLNLVYGDPAFTISP 339
 QY 423 SYTYRPGVNLNLSCHAASNPAPQYSWILDNINIOHTOELFISNITEKNSGLYTCQAHNS 482
 Db 340 STTYHSGENLNLSCFADSNPAPAYSWITNGAFQSLSGQTLFIPOITTKHSGLYACSVRNS 399
 QY 483 ASGHSRTTYKTTVSA 498
 Db 400 ATGMESSKSMYKVA 415

RESULT 11
 JC4123
 pregnancy-specific glycoprotein 7a precursor - human
 C:Species: Homo sapiens (man)
 C>Date: 26-Jul-1995 #sequence revision 19-Oct-1995 #text change 09-Jul-2004
 C:Accession: JC4123
 R:Reglund, S.; Zhou, G.Q.; Hammarstrom, S.
 Biochem. Biophys. Res. Commun. 211, 656-664, 1995
 A:Title: Characterization of cDNA encoding novel pregnancy-specific glycoprotein vari
 A:Reference number: JC4121; MUID:95314639; PMID:7794280
 A:Accession: JC4123
 A:Molecule type: mRNA
 A:Residues: 1-419 <TEG>
 A:Cross-references: UNIPROT:Q13046; UNIPARC:UPI00003327A2; GB:U18467; NID:g609313; PI
 A:Experimental source: fetal liver
 C:Comment: This protein belongs to the carcinoembryonic antigen family. This protein
 egnacy.
 C:Genetics:
 A:Gene: GDB:PSG7
 A:Cross-references: GDB:128241; OMIM:176396
 A:Map position: 19q13.2-19q13.2
 C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-term
 C:Keywords: glycoprotein
 F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
 F:1-34/Domain: signal sequence #status predicted <SIG>
 F:35-419/Product: pregnancy-specific glycoprotein 7a #status predicted <MAT>
 F:127-129/Region: cell attachment (R-G-D) motif
 F:162-219/Domain: immunoglobulin homology <IMM1>
 F:255-312/Domain: immunoglobulin homology <IMM2>

F:347-396/Domain: immunoglobulin homology <IMM3>
F:61,104,111,199,209,268,303/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 30.9%; Score 1148.5; DB 2; Length 419;
Best Local Similarity 48.1%; Pred. No. 2.6e-55;

Matches 238; Conservative 47; Mismatches 123; Indels 87; Gaps 3;

QY 5 SAPPHWCIPIWQRLITLTLASLLTFWNPPTTAKLTITESTPNNVAGKEVLLVNHLPQHLFG 64
DB 5 SAPPCQHIHWKGLLTLASLLTFWNPPTTAQVITEAPKPVSEKQVLLVNHLPQNLTG 64

QY 65 YSNYKGERVDGNROIIGYVIGTQOATPGPAVSGREIIPVNASLLIIONITQNTGFTYLAH 124
DB 65 YIYKQCIQIRDLHYHYSYVVDGQIIKYGPAVSGREIIPVNASLLIQNTGEDGSYTLHI 124

QY 125 IKSDLVNEBATQO--FRVYPELPKPSISNNSKPVEDKDAVAFTCEPEIQTATYLMVNN 182
DB 125 IKRGDGTGVTGFTFTLYLETPKPSISSNPNPREKTEAVIITCDPETHDASYLMWNG 184

QY 183 QSLPVPRLQSLNGNRTLLTFNVTNRNDTASVKCETQNPVSARRSDSVILNVLYGPDAPT 242
DB 185 QSLPMTSHLSQSLSTNRTLYFGVTNTYAGPYECEIRNPVSARSDDPTLNL----- 236

QY 243 SPLNTSYRSGENILNSCHAAASNPPAQSFWNGTFOOSTOELFIPNITVNNSSGYTQAH 302
DB 237 -----PKL----- 239

QY 303 NSDTGLNRTVTITTYAEPKPFITSSNSNPVEDDAVALTCEPEIQTATYLMVNN 362
DB 240 -----PKYITINLNPRENKDVSTFTCEPKSENYTYIMWLNQGS 279

QY 363 LPVSPRLQSLNDNRITLLSVTRNDVGPYECIQNELSYHSDPVLNVLYGPDPTISP 422
DB 280 LPVSPVKKRPIERILLISVTNRNETGYPQCEIRDRGIRSDPVTNLNVLYGPDLPRIY 339

QY 423 SYTYRPGVNLISCHAAASNPPAQSFWLIDGNIQHTQELFISNITEKNSGLYTQANN 482
DB 340 SFYHYSGENILYSCFADSNPPAQSFWTNGKFKQLSQKLSIPQITTKHSGLYACSVRNS 399

QY 483 ASGHSRTYVKTITVSA 497
DB 400 ATGESSKMTYKVAS 414

RESULT 12

157486

pregnancy-specific beta 1-glycoprotein - human

C/Species: Homo sapiens (man)

C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999

C/Accession: I57486

R/Shupert, W.L.; Chan, W.Y.

Mol. Cell. Biochem. 120, 159-170, 1993

A>Title: Pregnancy specific beta 1-glycoprotein in human intestine.

A/Reference number: I57486; MID:33254418; PMID:8487756

A/Accession: I57486

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-428 <RES>

A/Cross-references: UNIPARC:UPI0000073DC1; GB:SS9493; NID:g300090; PIDN:AC60584.1; PID:

C/Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-terminal

F/1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>

F/347-396/Domain: immunoglobulin homology <IMM>

Query Match 30.7%; Score 1141.5; DB 2; Length 428;

Best Local Similarity 47.4%; Pred. No. 6.4e-55;

Matches 225; Conservative 51; Mismatches 123; Indels 87; Gaps 3;

QY 5 SAPPHWCIPIWQRLITLTLASLLTFWNPPTTAKLTITESTPNNVAGKEVLLVNHLPQHLFG 64

DB 5 SAPPCQHIHWKGLLTLALINFWNLPTTAQVITEAPKPVSEKQVLLVNHLPQNLTG 64

QY 65 YSNYKGERVDGNROIIGYVIGTQOATPGPAVSGREIIPVNASLLIIONITQNTGFTYLAH 124

DB 65 YIYKQCIQIRDLHYHYSYVVDGQIIKYGPAVSGREIIPVNASLLIQNTREDGASYTLHI 124

QY 125 IKSDLVNEBATQO--FRVYPELPKPSISNNSKPVEDKDAVAFTCEPEIQTATYLMVNN 182
DB 125 IKRGDGTGVTGFTFTLYLETPKPSISSNYPREDMAVSLTCDPETHDASYLMWNG 184

QY 183 QSLPVPRLQSLNGNRTLLTFNVTNRNDTASVKCETQNPVSARRSDSVILNVLYGPDAPT 242
DB 185 QSLPMTSHLSQSLSTNRTLYFGVTNTYAGPYECEIRNPVSARSDDPTLNL----- 236

QY 243 SPLNTSYRSGENILNSCHAAASNPPAQSFWNGTFOOSTOELFIPNITVNNSSGYTQAH 302
DB 237 -----PKL----- 239

QY 303 NSDTGLNRTVTITTYAEPKPFITSSNSNPVEDDAVALTCEPEIQTATYLMVNN 362
DB 240 -----PKYITINLNPRENKDVSTFTCEPKSENYTYIMWLNQGS 279

QY 363 LPVSPRLQSLNDNRITLLSVTRNDVGPYECIQNELSYHSDPVLNVLYGPDPTISP 422
DB 280 LPVSPVKKRPIERILLISVTNRNETGYPQCEIRDRGIRSDPVTNLNVLYGPDLPRIY 339

QY 423 SYTYRPGVNLISCHAAASNPPAQSFWLIDGNIQHTQELFISNITEKNSGLYTQANN 482
DB 340 SFYHYSGENILYSCFADSNPPAQSFWTNGKFKQLSQKLSIPQITTKHSGLYACSVRNS 399

QY 483 ASGHSRTYVKTITVSA 498
DB 400 ATGESSKMTYKVAS 415

RESULT 13

A27658

pregnancy-specific beta-1 glycoprotein C precursor - human

C/Species: Homo sapiens (man)

C/Date: 31-Mar-1989 #sequence_revision 30-Jun-1991 #text_change 31-Oct-1997

C/Accession: A27658

R/Streydio, C.; Lacka, K.; Swillens, S.; Vassart, G.

Biochem. Biophys. Res. Commun. 154, 130-137, 1988

A>Title: The human pregnancy-specific beta-1-glycoprotein (PS-beta-G) and the carcinoem

A/Reference number: A27658; MID:88280756; PMID:3260773

A/Accession: A27658

A/Molecule type: mRNA

A/Residues: 1-428 <STR>

A/Cross-references: UNIPARC:UPI000006D843; GB:M19662

C/Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termi

F/1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>

F/35-428/Product: pregnancy-specific beta-1 glycoprotein C #status predicted <MT>

F/162-312/Domain: immunoglobulin homology <IMM1>

F/255-312/Domain: immunoglobulin homology <IMM2>

F/347-396/Domain: immunoglobulin homology <IMM3>

Query Match 30.5%; Score 1133.5; DB 2; Length 428;

Best Local Similarity 46.4%; Pred. No. 1.7e-54;

Matches 227; Conservative 56; Mismatches 131; Indels 87; Gaps 3;

QY 1 MESPSAPPHWCIPIWQRLITLTLASLLTFWNPPTTAKLTITESTPNNVAGKEVLLVNHLPQ 60
DB 1 MGLTAPPCQHIHWKGLLTLALINFWNLPTTAQVITEAPKPVSEKQVLLVNHLPQ 60

QY 61 HLFYKGERVDGNROIIGYVIGTQOATPGPAVSGREIIPVNASLLIIONITQNTGFTY 120
DB 61 NLTYIWKQMDLYHYTSYVVDGELIIPVAGSREIIPVNASLLIIONITQNTGFTY 120

QY 121 TLHVIKSDLVNEBATQO--FRVYPELPKPSISNNSKPVEDKDAVAFTCEPEIQTATYLM 178
DB 121 THIIKGDGTGVTGFTFTLYLETPKPSISSNLPRETEAVSLTCDPETHDASYLM 180

QY 179 WYNNQSLPVSRLQSLNGNRTLLTFNVTNRNDTASVKCETQNPVSARRSDSVILNVLYGPD 238
DB 179 YIYKQCIQIRDLHYHYSYVVDGQIIKYGPAVSGREIIPVNASLLIIONITQNTGFTYLAH 124

Db 181 MNQSLPMTHTSLKLETNRRLTLGLGVTKYTAGPYECEIRNPVSAERSDPVTLNLL----- 236

Qy 229 APTISPLMTSYKSGENLNLSCHAASNPQAQYMFVANGTFOQSTQELFINITVNNSGSYT 298

Db 237 -----PKL----- 239

Qy 239 COAHNSDTGLNRTVTITVVAEPKPFITSNNSNPVEDEDAVALTCEPEIGNTYLMMV 358

Db 240 -----PKYITINNLPREKDVANFTCEKSENYITIMVL 275

Qy 359 NNQSLPVSRLQSLNDNRITLLSVTRNDVGPYECGIONELSDHSDPVILNVLYGPDPP 418

Db 276 NQOSLPVSPRYKRPLENRLLPSVTRNETGPYQCEIRDRYGGINSDPVTLNVLYGPDLP 335

Qy 419 TISPSYTYRPGVNLSTLSCHAASNPQAQYMWLDIGNIQHTQELFTISNTEKNSGLYTCQ 478

Db 336 RIYSPFYTRSGEYVLYLSCSADSNPPAQSMTINEKFPQCKLFRHITTKHSGLYVCS 395

Qy 479 ANNSASGHSRTTVKTIIVASAELEPKPSISNN 509

Db 396 VRNSATGKSSKSMTEVSAVSSSINYISGN 426

RESULT 14

B55181

Pregnancy-specific beta-1-glycoprotein 11 form r precursor - human

C:Species: Homo sapiens (man)

C:Date: 23-Mar-1995 #sequence revision 23-Mar-1995 #text_change 31-Oct-1997

C:Accession: B55181

R:McNencham, P.A.; Rutherford, K.J.; Beggs, K.T.; Sims, S.E.; Mansfield, B.C.

Genomics 22, 356-363, 1994

A:Title: Characterization of the PSGL1 gene.

A:Reference number: A55181; MUID:95104046; PMID:7806221

A:Accession: B55181

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-436 <MCL>

A:Cross-references: UNIPARC:UPI00001770AC; GB:U04324

A:Gene: PSGL1

A:Cross-references: GDB:128242; OMIM:176398

A:Map position: 19q13.2-19q13.2

C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termi

F:1-138/Domain: alternative splicing; glycoprotein

F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>

F:255-312/Domain: immunoglobulin homology <IMM2>

Query Match 30.4%; Score 1130; DB 2; Length 436;

Best Local Similarity 46.9%; Pred. No. 2.8e-54;

Matches 236; Conservative 53; Mismatches 126; Indels 88; Gaps 5;

Qy 6 APPRWCIPQRLTLTASLTLTFMNPPTAKLTLESTPRVAVGKEVLLVHNLPQHLRGY 65

Db 6 APSCQRTWKGLLTASLTLTFMNPPTAKLTLESTPRVAVGKEVLLVHNLPQHLRGY 65

Qy 66 SWYGERVDGNKQIIGVITGQOATPGPAVSGREIIVPNASLLIIONTIQNTGTFTLAVI 125

Db 66 FWYGEWMDLYHYIISYIVDGKIIIVGPAVSGREIIVPNASLLIIONTRKAGTYTTHII 125

Qy 126 K-SPLVNEATG-OFRVYPELPPKPSISSNNSKPVVDKQAVAFCEPEPDATYLLVWVNO 183

Db 126 KRGETREIRHNFHTTLTLETPKPIYISSNLPFRAMEAVRLICDPETLDSYLLWMMNQ 185

Qy 184 SLVPSRLQSLNNGRTLLTFVTRNDTASVYKCETONPVSAERSDSVILNVLYGPDAPTIS 243

Db 186 SLPTVHRLQLSKTRRTLYLFGVTKYIAGPYECEIRNPVSAERSDPVTLNLL----- 236

Qy 244 PLNYSYRGENLNLSCHAASNPQAQYMFVANGTFOQSTQELFINITVNNSGSYTQAHN 303

Db 237 -----PKL----- 239

Qy 304 SDTGLNRTVTITVVAEPKPFITSNNSNPVEDEDAVALTCEPEIGNTYLMMVNO 363

Db 240 -----PIPYITINNLPREKDVANFTCEKSENYITIMVLNQSGL 280

Qy 364 PVSRLQSLNDRITLLSVTRNDVGPYECGIONELSDHSDPVILNVLYGPDPTISPS 423

Db 281 PVSPPGVKPIENRLLILPSVTRNETGPYQCEIRDRYGGINSNPVILNVLYGPDLPRIYPS 340

Qy 424 YTVYRPGVNLSTLSCHAASNPQAQYMWLDIGNIQHTQELFTISNTEKNSGLTQAHNSA 483

Db 341 FTYVYSGENLDSCTESPPPAEYFTTNGKFOQSGQKLFIPQITRNHSGLYACSVHNSA 400

Qy 484 SGHSRTTVKTIIVASAELEPKPSIS 506

Db 401 TCKEISKSMTEVSAVSSSINYISGN 422

RESULT 15

A35964

Pregnancy-specific glycoprotein I form d precursor - human

N:Alternate names: pregnancy-specific beta-1 glycoprotein 95; pregnancy-specific beta-

C:Species: Homo sapiens (man)

C:Date: 09-Nov-1990 #sequence revision 09-Nov-1990 #text_change 31-Oct-1997

C:Accession: A35964; B35964; B43354

R:Leslie, K.K.; Matanabe, S.; Lei, K.J.; Chou, D.Y.; Plouzek, C.A.; Deng, H.C.; Torres

Proc. Natl. Acad. Sci. U.S.A. 87, 5822-5826, 1990

A:Title: Linkage of two human pregnancy-specific beta-1-glycoprotein genes: one is ess

A:Reference number: A35964; MUID:90332674; PMID:2377620

A:Accession: A35964

A:Molecule type: mRNA

A:Residues: 1-426 <LES>

A:Cross-references: UNIPARC:UPI000017709B; GB:M34715

A:Accession: B35964

A:Molecule type: DNA

A:Residues: 237-426 <LE2>

A:Cross-references: UNIPARC:UPI000017709F; GB:M34716

R:lei, K.J.; Sartwell, A.D.; Pan, C.J.; Chou, J.Y.

J. Biol. Chem. 267, 16371-16378, 1992

A:Title: Cloning and expression of genes encoding human pregnancy-specific glycoprotei

A:Reference number: A43354; MUID:92355602; PMID:1644821

A:Accession: B43354

A:Molecule type: DNA

A:Residues: 23-426 <LE1>

A:Cross-references: UNIPARC:UPI00001770A0

A:Note: sequence extracted from NCBI backbone (NCBIN:110710, NCBIN:110714, NCBIN:11071

C:Genetics:

A:Gene: PSGL1

A:Cross-references: GDB:120321; OMIM:176390

A:Map position: 19q13.2-19q13.2

A:Introns: 122/1; 215/1; 308/1

C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termi

F:1-138/Domain: alternative splicing; glycoprotein

F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>

F:162-219/Domain: immunoglobulin homology <IMM1>

F:255-312/Domain: immunoglobulin homology <IMM2>

F:347-396/Domain: immunoglobulin homology <IMM3>

Query Match 30.3%; Score 1127.5; DB 2; Length 426;

Best Local Similarity 46.7%; Pred. No. 3.7e-54;

Matches 234; Conservative 55; Mismatches 125; Indels 87; Gaps 3;

Qy 1 MESPAPEHRWCIPQRLTLTASLTLTFMNPPTAKLTLESTPRVAVGKEVLLVHNLPQ 60

Db 1 MGTISAPPCQRIKWKGLLTASLTLTFMNPPTAKLTLESTPRVAVGKEVLLVHNLPQ 60

Qy 61 HLFGYSYKGRVDGNKQIIGVITGQOATPGPAVSGREIIVPNASLLIIONTIQNTGTFTLAVI 120

Db 61 NLGTGYIMYKGMRLDLYHYIISYIVDGKIIIVGPAVSGREIIVPNASLLIIONTRKAGTYTTHII 120

Qy 121 TLVYKSLVNEATG--FRVYPELPPKPSISSNNSKPVVDKQAVAFCEPEPDATYLLVWVNO 178

Db 121 TLHIIKGDGTGRVYGRFTTLTLETPKPIYISSNLPFRAMEAVRLICDPETLDSYLLWMMNQ 180

Qy 179 WVNQSLPVSRLQSLNNGRTLLTFVTRNDTASVYKCETONPVSAERSDSVILNVLYGPD 238

```
Db      181 MNNGSLPMTHTSLKSETNRTLLFLGVTKYTAGPYECEIRNPVSASRSDPVTLLNL---- 236
Qy      239 APTISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFOQSTQELFIPNITVNNGSYT 298
Db      237 -----PKL----- 239
Qy      299 COAHNSDTGLNRTTVTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIONTTYLMVY 358
Db      240 -----PKPYITINLNPRENKDVLNFTCEPKSENYIYIMWL 275
Qy      359 NNOSLPVSPRLQSLNDRRTLLSVTRNDVGPYECIQNELSYDHSDPVILNVLYGPDDE 418
Db      276 NGOSLPVSPRVKPKPIENRILILPSVTRNETGPYQCEIRDRYGGVRSDPVTLLNVLYGPDLE 335
Qy      419 TISPSYTYRPGVNLISLSCHAASNPPAQYSWMLIDGNIQOHTOELFISNITEKNSGLYTQ 478
Db      336 RIYPSFTYRSGEVLILSCSADSNPPAQYSWMTINEKPOLPGOKLFI RHITTHSGLYVCS 395
Qy      479 ANNSAGHSRTTVKITTVSAAE 499
Db      396 VRNSATGKESKSMTEVVS GK 416
```

Search completed: April 10, 2006, 18:07:34
Job time : 42.1584 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: April 10, 2006, 17:55:34 ; Search time 237.861 Seconds

(without alignments)
2082.225 Million cell updates/sec

Title: US-10-734-564-72

Perfect score: 3721
Sequence: 1 MESPSAPPHRMCIPIWQRLLL.....LSAGATVGMIGLVGVALLI 702

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80:*
1: uniprot_sprot:*
2: uniprot_crembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3721	100.0	702	1	CEAM5_HUMAN
2	3717	99.9	702	2	Q8W4D0_HUMAN
3	3713	99.8	702	2	Q53G30_HUMAN
4	2066	55.5	420	2	Q68DM9_HUMAN
5	1609	43.2	526	1	CEAM1_HUMAN
6	1600.5	43.0	464	2	Q16170_HUMAN
7	1600.5	43.0	464	2	Q96CA7_HUMAN
8	1526.5	41.0	525	2	Q5R9N6_PONPY
9	1470	39.5	287	2	Q13984_HUMAN
10	1443	38.8	344	1	CEAM6_HUMAN
11	1443	38.8	344	2	Q53XP7_HUMAN
12	1443	38.8	344	2	Q13774_HUMAN
13	1426.5	38.3	368	2	Q5UBA9_HUMAN
14	1423	38.2	461	2	Q13854_HUMAN
15	1272	34.2	349	1	CEAM8_HUMAN
16	1194.5	32.1	373	1	Q7KXPS_HUMAN
17	1157.5	31.1	428	1	PSG3_HUMAN
18	1148.5	30.9	419	1	PSG7_HUMAN
19	1141.5	30.7	428	2	Q9HRM2_HUMAN
20	1140.5	30.5	426	1	PSG8_HUMAN
21	1134.5	30.3	419	2	Q68CR6_HUMAN
22	1127.5	30.3	426	2	Q61CR4_HUMAN
23	1126.5	30.3	419	1	PSG1_HUMAN
24	1126.5	30.3	426	1	PSG9_HUMAN
25	1125.5	30.2	426	2	Q6LEU7_HUMAN
26	1124.5	30.2	411	2	Q15228_HUMAN
27	1118.5	30.1	419	2	Q96QUS_HUMAN
28	1117.5	30.0	419	2	Q6P520_HUMAN
29	1114.5	30.0	419	1	PSG4_HUMAN
30	1107.5	29.8	435	1	PSG6_HUMAN
31	1104	29.7	424	1	PSG10_HUMAN

32	1070.5	28.8	521	2	Q61352_MOUSE
33	1065.5	28.6	458	2	Q61351_MOUSE
34	1023.5	27.5	521	1	CEAM1_MOUSE
35	1023.5	27.5	521	2	Q925P3_MOUSE
36	1018.5	27.4	454	2	Q91W54_MOUSE
37	998	26.8	520	2	Q925P2_MOUSE
38	992	26.7	459	2	Q9JHL6_RAT
39	983	26.4	458	2	Q63093_RAT
40	980	26.3	448	2	Q9JHL7_RAT
41	970.5	26.1	519	1	CEAM1_RAT
42	919	24.7	402	2	Q15227_HUMAN
43	901.5	24.2	352	2	Q15403_HUMAN
44	900.5	24.2	352	2	Q08266_HUMAN
45	898	24.1	332	1	PSG11_HUMAN

ALIGNMENTS

RESULT 1	ID	CEAM5_HUMAN	STANDARD;	PRT;	702 AA.
AC	P06731;				
DT	01-JAN-1988 (Rel. 06, Created)				
DT	01-DEC-1992 (Rel. 24, Last sequence update)				
DT	10-MAY-2005 (Rel. 47, Last annotation update)				
DE	Carcinoembryonic antigen-related cell adhesion molecule 5 precursor				
DE	(Carcinoembryonic antigen) (CEA) (Meconium antigen 100) (CD66e antigen).				
GN	Name=CEACAM5; Synonyms=CEA;				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;				
OC	Hom.				
RN	NCBI_TaxID=9606;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RX	MEDLINE=90258861; PubMed=2342461; Hefla L.J.F., Maruya A.,				
RA	Schrewe H., Thompson J., Bona M.,				
RA	Hassauer M., Shively J.B., von Kleist S., Zimmermann W.,				
RT	"Cloning of the complete gene for carcinoembryonic antigen: analysis of its promoter indicates a region conveying cell type-specific expression."				
RT	Mol. Cell. Biol. 10:2738-2748(1990).				
RL	[2]				
RP	NUCLEOTIDE SEQUENCE.				
RX	MEDLINE=88038876; PubMed=3670312; Beauchemin N., Benichou S., Cournoyer D., Fuks A., Stanners C.P.,				
RA	"Isolation and characterization of full-length functional cDNA clones for human carcinoembryonic antigen."				
RT	Mol. Cell. Biol. 7:3221-3230(1987).				
RL	[3]				
RP	NUCLEOTIDE SEQUENCE.				
RX	MEDLINE=89122014; PubMed=3220478; Barnett T., Geobel S.J., Notdurft M.A., Elting J.J.,				
RA	"Carcinoembryonic antigen family: characterization of cDNAs coding for NCA and CEA and suggestion of nonrandom sequence variation in their conserved loop-domains."				
RT	Genomics 3:59-66(1988).				
RL	[4]				
RP	NUCLEOTIDE SEQUENCE OF 5-702.				
RX	MEDLINE=87128144; PubMed=3814146; Oikawa S., Nakazato H., Kosaki G.,				
RA	"Primary structure of human carcinoembryonic antigen (CEA) deduced from cDNA sequence."				
RT	Biochem. Biophys. Res. Commun. 142:511-518(1987).				
RL	[5]				
RP	NUCLEOTIDE SEQUENCE OF 331-702.				
RX	MEDLINE=87204247; PubMed=3033671; Zimmermann W., Ottlieb B., Friedrich R., von Kleist S.,				
RA	"Isolation and characterization of cDNA clones encoding the human carcinoembryonic antigen reveal a highly conserved repeating structure."				
RT					

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 NCBI_TaxId=9606;
 [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=colon;
 RX MEDLINE=2238257; PubMed=12479732; DOI=10.1073/pnas.242603899;
 RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Altschuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stancovski M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carminci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., Melwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultky S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=colon;
 RA Strausberg R.;
 CC Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC034671; AAH34671.1; -; mRNA.
 DR HSSP; Q61353; 1L62.
 DR Ensemble; ENSG00000105388; Homo sapiens.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_c2.
 DR Pfam; PF00047; ig_6.
 DR SMART; SM00408; IGc2; 3.
 DR PROSITE; PS50835; IG_LIKE; 6.
 KW Immunoglobulin domain; Transmembrane.
 SQ SEQUENCE 702 AA; 76782 MW; 97CCFB7399A0B05A CRC64;

Query Match 99.9%; Score 3717; DB 2; Length 702;
 Best Local Similarity 99.9%; Pred. No. 1e-203;
 Matches 701; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESPAPRRNCIPWQRLTLTASLTTFNNPPTAKLTTESTPFFNVAEGEVLVHNPQ 60
 DB 1 MESPAPRRNCIPWQRLTLTASLTTFNNPPTAKLTTESTPFFNVAEGEVLVHNPQ 60
 QY 61 HLFQSWYKGERVDGNROIIIGVIGTQOATGPAYSGREIIPNASSLIQNIQNDTGFY 120
 DB 61 HLFQSWYKGERVDGNROIIIGVIGTQOATGPAYSGREIIPNASSLIQNIQNDTGFY 120
 QY 121 TLHVKSDLVNBEATGQFRVYPPELPKPSISSNNSKPVEDKDAVAFTCEPQTODATYLMWV 180
 DB 121 TLHVKSDLVNBEATGQFRVYPPELPKPSISSNNSKPVEDKDAVAFTCEPQTODATYLMWV 180
 QY 181 NNOSLPVSPRLOLSNGRNTLTFTNTRNDTASYKCEIQNPVSARSDSVILNLYGPDAP 240
 DB 181 NNOSLPVSPRLOLSNGRNTLTFTNTRNDTASYKCEIQNPVSARSDSVILNLYGPDAP 240
 QY 241 TISPLNTSYRSGENINLSCHAASNPAPQYSWFGNGTFOOSTQELFIPNITVNNSSGYCQ 300
 DB 241 TISPLNTSYRSGENINLSCHAASNPAPQYSWFGNGTFOOSTQELFIPNITVNNSSGYCQ 300
 QY 301 AHSNPTGLNRTTITTTTYYAEPKPFITSSNNSPVEDDAVALICEPEIQNTTYLWVNN 360
 DB 301 AHSNPTGLNRTTITTTTYYAEPKPFITSSNNSPVEDDAVALICEPEIQNTTYLWVNN 360
 QY 301 AHSNPTGLNRTTITTTTYYAEPKPFITSSNNSPVEDDAVALICEPEIQNTTYLWVNN 360
 DB 301 AHSNPTGLNRTTITTTTYYAEPKPFITSSNNSPVEDDAVALICEPEIQNTTYLWVNN 360

QY 361 QSLVPSRQLQSNDRNTLTLSVTRNDVGEYCEGIONELSDHSDPVIILNLYGPDPTI 420
 DB 361 QSLVPSRQLQSNDRNTLTLSVTRNDVGEYCEGIONELSDHSDPVIILNLYGPDPTI 420
 QY 421 SPSYTYRPGVNLISCHAASNPAPQYSWFLDGNITQOHTQELFISNITERKNSGLYTCQAN 480
 DB 421 SPSYTYRPGVNLISCHAASNPAPQYSWFLDGNITQOHTQELFISNITERKNSGLYTCQAN 480
 QY 481 NSASGHSRTTYVTITYSALPSPSISNNSKVEDKDAVAFTCEPAQNTTYLWVNGQS 540
 DB 481 NSASGHSRTTYVTITYSALPSPSISNNSKVEDKDAVAFTCEPAQNTTYLWVNGQS 540
 QY 541 LVPSPRLQSNDRNTLTFTNTRNDARAVYCGIQQSVSANSRDPVTLVLYGPDPTISP 600
 DB 541 LVPSPRLQSNDRNTLTFTNTRNDARAVYCGIQQSVSANSRDPVTLVLYGPDPTISP 600
 QY 601 PDSYLSGANLNLISCHASNPSPQYSWRINGIPQOHTQVLTAKITPNNNGYACFVSNL 660
 DB 601 PDSYLSGANLNLISCHASNPSPQYSWRINGIPQOHTQVLTAKITPNNNGYACFVSNL 660
 QY 661 ATGRNNSIVKSTTVSAGTSPGLSAGATVIGIVGVYAL 702
 DB 661 ATGRNNSIVKSTTVSAGTSPGLSAGATVIGIVGVYAL 702

RESULT 3
 Q53G30 HUMAN
 ID Q53G30 HUMAN PRELIMINARY; PRT; 702 AA.
 AC Q53G30;
 DT 13-SEP-2005 (TRENBLREL. 31, Created)
 DT 13-SEP-2005 (TRENBLREL. 31, Last sequence update)
 DT 13-SEP-2005 (TRENBLREL. 31, Last annotation update)
 DE Carcinoembryonic antigen-related cell adhesion molecule 5 variant
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 NCBI_TaxId=9606;
 [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Maruyama K., Sugano S.;
 RT "Oligo-capping: a simple method to replace the cap structure of
 RT eucaryotic mRNAs with oligoribonucleotides.";
 RL Gene 138:171-174(1994).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Suzuki Y., Yoshitomo K., Maruyama K., Suyama A., Sugano S.;
 RT "Construction and characterization of a full length-enriched and a 5'-
 RT end-enriched cDNA library.";
 RL Gene 200:149-156(1997).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki Y.,
 RA Tanaka A., Yokoyama S., to the EMBL/GenBank/DBJ databases.
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK223101; BAD96821.1; -; mRNA.
 FT NON TER 1
 SQ SEQUENCE 702 AA; 76867 MW; 62992426CDDAB5C CRC64;

Query Match 99.8%; Score 3713; DB 2; Length 702;
 Best Local Similarity 99.9%; Pred. No. 1.7e-203;
 Matches 701; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MESPAPRRNCIPWQRLTLTASLTTFNNPPTAKLTTESTPFFNVAEGEVLVHNPQ 60
 DB 1 MESPAPRRNCIPWQRLTLTASLTTFNNPPTAKLTTESTPFFNVAEGEVLVHNPQ 60
 QY 61 HLFQSWYKGERVDGNROIIIGVIGTQOATGPAYSGREIIPNASSLIQNIQNDTGFY 120
 DB 61 HLFQSWYKGERVDGNROIIIGVIGTQOATGPAYSGREIIPNASSLIQNIQNDTGFY 120
 QY 121 TLHVKSDLVNBEATGQFRVYPPELPKPSISSNNSKPVEDKDAVAFTCEPQTODATYLMWV 180
 DB 121 TLHVKSDLVNBEATGQFRVYPPELPKPSISSNNSKPVEDKDAVAFTCEPQTODATYLMWV 180

```

|||||
Db 121 TLHVKISDLVNEBATOQFRVYPPELPKPSISSNNSKVEDKDAVAFCEPETQDATYLMVY 180
Qy 181 NNOSLPVSPRLQSLNSGNRTLTLENTVRNDTASVKCTONPVARSBSVLIINVLXGPDPA 240
Db 181 NNOSLPVSPRLQSLNSGNRTLTLENTVRNDTASVKCTONPVARSBSVLIINVLXGPDPA 240
Qy 241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWPFVNGTFOOSTOELFIPNITVNNSGSYTCQ 300
Db 241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWPFVNGTFOOSTOELFIPNITVNNSGSYTCQ 300
Qy 301 AHNSDTGLNRTTITTYTVAEPKPFITSNNSNPVEDDAVALTCEPEIQNTTYLMMVNN 360
Db 301 AHNSDTGLNRTTITTYTVAEPKPFITSNNSNPVEDDAVALTCEPEIQNTTYLMMVNN 360
Qy 361 QSLPVSPRLQSLNSGNRTLTLENTVRNDVGPYECGIONELSDVSHSDVLIINVLXGPDPTI 420
Db 361 QSLPVSPRLQSLNSGNRTLTLENTVRNDVGPYECGIONELSDVSHSDVLIINVLXGPDPTI 420
Qy 421 SPSTYYRPGVNLNLSCHAASNPPAQYSWMLIDGNIQOHTOELFISNTEKNSGLYTCQAN 480
Db 421 SPSTYYRPGVNLNLSCHAASNPPAQYSWMLIDGNIQOHTOELFISNTEKNSGLYTCQAN 480
Qy 481 NSASGHSRTTVKTIIVSAELPKPSISSNNSKPEDKDAVAFCEPEAQNTTYLMMVNGOS 540
Db 481 NSASGHSRTTVKTIIVSAELPKPSISSNNSKPEDKDAVAFCEPEAQNTTYLMMVNGOS 540
Qy 541 LPPSPRLQSLNSGNRTLTLENTVRNDARAYVCGIONSVSANSDPVLTVLXGPDPTIIS 600
Db 541 LPPSPRLQSLNSGNRTLTLENTVRNDARAYVCGIONSVSANSDPVLTVLXGPDPTIIS 600
Qy 601 PDSSYLSGANLNLSCHASNPSPQYSWRINGIPQOHTOVLFIKATIPNNNGTACVFSVNL 660
Db 601 PDSSYLSGANLNLSCHASNPSPQYSWRINGIPQOHTOVLFIKATIPNNNGTACVFSVNL 660
Qy 661 ATGRNNSIVKSIIVSASGTSPELSAGATVGIMIGLVGVALLI 702
Db 661 ATGRNNSIVKSIIVSASGTSPELSAGATVGIMIGLVGVALLI 702

RESULT 4
ID 068DM9 HUMAN PRELIMINARY; PRT; 420 AA.
AC 068DM9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein DKFZp781M2392.
GN Name=DKFZp781M2392;
OS Homo sapiens (Human) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RA NUCLEOTIDE SEQUENCE.
RC TISSUE=Colon carcinoma;
RG The German cDNA Consortium;
RA Poustka A., Albert R., Woosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amlid C., Osaenger A., Fobio G., Han M., Wiemann S.;
RA Submitted (Aug-2004) to the EMBL/GenBank/DBJ databases.
DE EMBL: CR749337; CAH18191.1; -; mRNA.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003598; IG_c2.
DR Pfam: PF00047; IG_3.
DR SMART: SM00409; IG2; 3.
DR SMART: SM00408; IG2; 3.
DR PROSITE: PS00835; IG_LIKE; 3.
KM Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 420 AA; 45508 MW; 6E30C0BA00D0F59 CRC64;

Query Match 55.5%; Score 2066; DB 2; Length 420;

```

```

Best Local Similarity 59.8%; Pred. No. 7.5e-110;
Matches 420; Conservative 0; Mismatches 0; Indels 282; Gaps 1;

Qy 1 MESSAPAPPRWCIIPQORLLTTSILTFPNNPPTAKLTIESPPENVAEKEVLLVHNLPQ 60
Db 1 MESSAPAPPRWCIIPQORLLTTSILTFPNNPPTAKLTIESPPENVAEKEVLLVHNLPQ 60
Qy 61 HLFQSWYKGEVDNQRQIIGVIGTQOATGPAVSGREIIYPNASLLIQNIQNDGFFY 120
Db 61 HLFQSWYKGEVDNQRQIIGVIGTQOATGPAVSGREIIYPNASLLIQNIQNDGFFY 120
Qy 121 TLHVKISDLVNEBATOQFRVYPPELPKPSISSNNSKVEDKDAVAFCEPETQDATYLMVY 180
Db 121 TLHVKISDLVNEBATOQFRVYPPELPKPSISSNNSKVEDKDAVAFCEPETQDATYLMVY 180
Qy 181 NNOSLPVSPRLQSLNSGNRTLTLENTVRNDTASVKCTONPVARSBSVLIINVLXGPDPA 240
Db 181 NNOSLPVSPRLQSLNSGNRTLTLENTVRNDTASVKCTONPVARSBSVLIINVLXGPDPA 240
Qy 241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWPFVNGTFOOSTOELFIPNITVNNSGSYTCQ 300
Db 241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWPFVNGTFOOSTOELFIPNITVNNSGSYTCQ 300
Qy 301 AHNSDTGLNRTTITTYTVAEPKPFITSNNSNPVEDDAVALTCEPEIQNTTYLMMVNN 360
Db 301 AHNSDTGLNRTTITTYTVAEPKPFITSNNSNPVEDDAVALTCEPEIQNTTYLMMVNN 360
Qy 361 QSLPVSPRLQSLNSGNRTLTLENTVRNDVGPYECGIONELSDVSHSDVLIINVLXGPDPTI 420
Db 361 QSLPVSPRLQSLNSGNRTLTLENTVRNDVGPYECGIONELSDVSHSDVLIINVLXGPDPTI 420
Qy 421 SPSTYYRPGVNLNLSCHAASNPPAQYSWMLIDGNIQOHTOELFISNTEKNSGLYTCQAN 480
Db 421 SPSTYYRPGVNLNLSCHAASNPPAQYSWMLIDGNIQOHTOELFISNTEKNSGLYTCQAN 480
Qy 481 NSASGHSRTTVKTIIVSAELPKPSISSNNSKPEDKDAVAFCEPEAQNTTYLMMVNGOS 540
Db 481 NSASGHSRTTVKTIIVSAELPKPSISSNNSKPEDKDAVAFCEPEAQNTTYLMMVNGOS 540
Qy 541 LPPSPRLQSLNSGNRTLTLENTVRNDARAYVCGIONSVSANSDPVLTVLXGPDPTIIS 600
Db 541 LPPSPRLQSLNSGNRTLTLENTVRNDARAYVCGIONSVSANSDPVLTVLXGPDPTIIS 600
Qy 601 PDSSYLSGANLNLSCHASNPSPQYSWRINGIPQOHTOVLFIKATIPNNNGTACVFSVNL 660
Db 601 PDSSYLSGANLNLSCHASNPSPQYSWRINGIPQOHTOVLFIKATIPNNNGTACVFSVNL 660
Qy 661 ATGRNNSIVKSIIVSASGTSPELSAGATVGIMIGLVGVALLI 702
Db 661 ATGRNNSIVKSIIVSASGTSPELSAGATVGIMIGLVGVALLI 702

RESULT 5
ID CEAMI HUMAN STANDARD; PRT; 526 AA.
AC P13688; O60430; Q13858; Q15600; Q9UQV9;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 13-SEP-2003 (Rel. 48, Last annotation update)
DE Carcinomembryonic antigen-related cell adhesion molecule 1 precursor
DE (Biliary glycoprotein 1) (BCP-1) (Antigen CD66) (CD66a antigen) .
GN Name=CEACAM1; Synonyms=BCP, BGP1;
OS Homo sapiens (Human) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RA NUCLEOTIDE SEQUENCE (ISOPFORM A), AND PARTIAL PROTEIN SEQUENCE.
RC MEDLINE=8832055; PubMed=2457922;
RA Hinoda Y., Neumaier M., Hefla S.A., Drzeniek Z., Wagnener C.,
RA Shively L., Hefla L.J.F., Shively J.B., Paxton R.J.;
RT "Molecular cloning of a cDNA coding biliary glycoprotein I: primary

```

RT structure of a glycoprotein immunologically crossreactive with
 RT carcinoembryonic antigen.";
 RA Proc. Natl. Acad. Sci. U.S.A. 85:6959-6963(1988).
 RN [2]
 RP ERATUM, AND SEQUENCE REVISION.
 RA Hinoda Y., Neumaler M., Hetta S.A., Drzeniek Z., Wagener C.,
 RA Shively L., Hetta L.J.F., Shively J.E., Paxton R.J.;
 RA Proc. Natl. Acad. Sci. U.S.A. 86:1668-1668(1989).
 RN [3]
 RP NUCLEOTIDE SEQUENCE (ISOFORMS A AND B).
 RX MEDLINE=89139550; PubMed=2537311; DOI=10.1083/jcb.108.2.267;
 RA Barnett T.R., Ketschmer A., Austen D.A., Goebel S.J., Hart J.T.,
 RA Elting J.J., Kamat M.B.;
 RT "Carcinoembryonic antigens: alternative splicing accounts for the
 RT multiple mRNAs that code for novel members of the carcinoembryonic
 RT antigen family.";
 RL J. Cell Biol. 108:267-276(1989).
 RN [4]
 RP NUCLEOTIDE SEQUENCE (ISOFORMS A; B; C; G; H AND I).
 RC TISSUE=Leukocyte;
 RX MEDLINE=91222219; PubMed=2025273;
 RA Kuroki M., Arakawa F., Matsuo Y., Oikawa S., Nakazato H., Matsuka Y.;
 RT "Three novel molecular forms of biliary glycoprotein deduced from cDNA
 RT clones from a human leukocyte library.";
 RL Biochem. Biophys. Res. Commun. 176:578-585(1991).
 RN [5]
 RP NUCLEOTIDE SEQUENCE (ISOFORM D).
 RX MEDLINE=93140765; PubMed=8423792;
 RA Barnett T.R., Drake L., Pickle W. II;
 RT "Human biliary glycoprotein gene: characterization of a family of
 RT novel alternatively spliced RNAs and their expressed proteins.";
 RL Mol. Cell. Biol. 13:1273-1282(1993).
 RN [6]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX PubMed=15057824; DOI=10.1038/nature02399;
 RA Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J.,
 RA Lamerdin J.E., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M.,
 RA Aerts A., Altherr M., Ashworth L., Bajorek E., Black S., Branscomb E.,
 RA Caenepeel S., Carraro A.V., Coile C., Chan Y.M., Christensen M.,
 RA Cleland C.A., Copeland A., Dalin B., Delai P., Denny J.C.,
 RA Escobar J., Flowers D., Fotopoulos D., Garcia C., Georgescu A.M.,
 RA Glavina T., Gomez M., Gonzales E., Groza M., Hammon N., Hawkins T.,
 RA Haydu L., Ho I., Huang W., Irsani S., Jett J., Kader K., Kimball H.,
 RA Kobayashi A., Larionov V., Leem S.-H., Lopez F., Lou Y., Lowry S.,
 RA Malfaceti S., Martinez D., McCreedy P.M., Medina C., Morgan J.,
 RA Nelson K., Nolan M., Ovcharenko I., Pfluck S., Pollard M.,
 RA Poppe A.P., Predki P., Quan G., Ramirez L., Rash S., Retterer J.,
 RA Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D.,
 RA Slezak T., Solovyev V., Thayer N., Tice H., Tsai M., Ustaszewska A.,
 RA Vo N., Wagner M., Wheeler J., Wu K., Xie G., Yang J., Dubchak I.,
 RA Purey T.S., DeJong P., Dickson M., Gordon D., Eichler E.E.,
 RA Pennacchio L.A., Richardson P., Stubbs L., Rokhsar D.S., Myers R.M.,
 RA Rubin E.M., Lucas S.M.;
 RT "The DNA sequence and biology of human chromosome 19.";
 RL Nature 428:529-535(2004).
 RN [7]
 RP NUCLEOTIDE SEQUENCE OF 1-21, AND DISEASE.
 RX MEDLINE=94333343; PubMed=8055923;
 RA Hauck W., Nedellec P., Turbide C., Stanners C.P., Barnett T.R.,
 RA Beauchemin N.;
 RT "Transcriptional control of the human biliary glycoprotein gene, a CEA
 RT gene family member down-regulated in colorectal carcinomas.";
 RL Eur. J. Biochem. 223:529-541(1994).
 RN [8]
 RP NUCLEOTIDE SEQUENCE OF 1-21.
 RX MEDLINE=95354678; PubMed=7628460;
 RA Nedellec P., Turbide C., Beauchemin N.;
 RT "Characterization and transcriptional activity of the mouse biliary
 RT glycoprotein 1 gene, a carcinoembryonic antigen-related gene.";
 RL Eur. J. Biochem. 231:104-114(1995).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoform A, isoform
 CC B and isoform C). Secreted (isoform G, isoform H and isoform I).
 CC -1- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=7;
 CC Name=A;
 CC IsoId=P13688-1; Sequence=Displayed;
 CC Name=G;
 CC IsoId=P13688-2; Sequence=VSP_002482, VSP_002483;
 CC Name=H;
 CC IsoId=P13688-3; Sequence=VSP_002478, VSP_002479;
 CC Name=I;
 CC IsoId=P13688-4; Sequence=VSP_002480, VSP_002481;
 CC Name=B;
 CC IsoId=P13688-5; Sequence=VSP_009227;
 CC Name=C;
 CC IsoId=P13688-6; Sequence=VSP_010938;
 CC Name=D;
 CC IsoId=P13688-7; Sequence=VSP_012222;
 CC -1- DISEASE: Loss or reduced expression is a major event in colorectal
 CC carcinogenesis.
 CC -1- DISEASE: Increased serum levels of BGP-1 are found in individuals
 CC suffering from hepatic disorders.
 CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily CEA family.
 CC -1- SIMILARITY: Contains 3 Ig-like C2-type (immunoglobulin-like)
 CC domains.
 CC -1- SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like)
 CC domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL, J03658; AAAS1826.1; -; mRNA.
 CC EMBL, X16354; CAA34404.1; -; mRNA.
 CC EMBL, D90311; BAA14341.1; -; mRNA.
 CC EMBL, D90312; BAA14342.1; -; mRNA.
 CC EMBL, D90313; BAA14343.1; -; mRNA.
 CC EMBL, X14831; CAA32940.1; -; mRNA.
 CC EMBL, M69176; AAAS1825.1; -; mRNA.
 CC EMBL, M72238; AAAS8393.1; -; mRNA.
 CC EMBL, M72238; AAAS8394.1; -; mRNA.
 CC EMBL, M76742; AAAS7142.1; -; mRNA.
 CC EMBL, AC004785; AAC18433.1; -; Genomic DNA.
 CC EMBL, AC004785; AAC18434.1; -; Genomic DNA.
 CC EMBL, AC004785; AAC18435.1; -; Genomic DNA.
 CC EMBL, AC004785; AAC18437.1; -; Genomic DNA.
 CC EMBL, AC004785; AAC18439.1; -; Genomic DNA.
 CC EMBL, X67277; CAA47694.1; -; Genomic DNA.
 CC PIR, A32164; A32164.
 CC PIR, JH0394; JH0394.
 CC PIR, JH0395; JH0395.
 CC PIR, JH0396; JH0396.
 CC HSSP, Q61353; 116Z.
 CC DR Ensembl, ENSG00000079385; Homo sapiens.
 CC DR HGN, HGNC:1814; CEACAM1.
 CC MIM, 109770; -;
 CC GO, GO:0005887; C:integral to plasma membrane, NAS.
 CC GO, GO:0005624; C:membrane fraction, TAS.
 CC GO, GO:0001525; P:angiogenesis, NAS.
 CC GO, GO:0016477; P:cell migration, NAS.
 CC GO, GO:0007156; P:homophilic cell adhesion, NAS.
 CC GO, GO:0007229; P:integrin-mediated signaling pathway, NAS.
 CC GO, GO:0007565; P:pregnancy, TAS.
 CC InterPro, IPR007110; Ig-like.
 CC InterPro, IPR003598; Ig_c2.
 CC Pfam, PF00047; Ig_3.
 CC SMART, SM00408; IGC2; 2.
 CC PROSITE, PS00835; IG_LIKE; 3.
 CC Alternative splicing; Direct protein sequencing; Glycoprotein;
 CC Immunoglobulin domain; Pyrolydine carboxylic acid; Repeat; Signal;
 CC Transmembrane.
 CC CHAIN 1 34 Carcinoembryonic antigen-related cell

	Query Match	43.0%;	Score 1600.5;	DB 2;	Length 468;
	Best Local Similarity	73.0%;	Pred. No. 3e-83;		
	Matches 309;	Conservative 30;	Mismatches 79;	Indels 5;	Gaps 2;
OY	SAPHRMVICPQRIILLTASLLTFNNPPPTAKLTATSTSPVNAEGKEVLIVHNLPOHLFG 64	:	:	:	:
Db	SAPLHRVRVPQGILLTRSLITFPNPTTAQLTTESHPFVAEGKEVLILVHNLPOOLFG 64	:	:	:	:
OY	YSWKGERVDGNROIIGVIGTGQAATGPAYSGREIIYPNASLLIQNIQNDFGYTLAV 124	:	:	:	:
Db	YSWKGEERVDNRQIIGVYAIGTQAATGPGANSGETEYIPNASLLIQNVTONDGFYTLQV 124	:	:	:	:
OY	IKSLDVNEAAGCGRRVPELPKPSISNNSSKPVEDKDAVAFCTGEPFODATYLMMVNOS 184	:	:	:	:
Db	IKSLDVNEEAAGCHVYPELPKPSISNNNSNPEDKAVALFTCEPFODTTYLMWINNOS 184	:	:	:	:
OY	LPLVSPRLQLSNGNFLLLFNTVRNDVTASYKCETONPVSAARSDSVLIANTVYGDPATISP 244	:	:	:	:
Db	LPLVEPRQLQSLNGNFTLLSTVRNDGTPEYCEIIONPVSAARSDPYLIANTVYGGPTTISP 244	:	:	:	:
OY	245 LNTSYRSGENINLSCHAASNPPAQYSFVNGTPQOSTOELFIPIITVNNSGSYTCQAHNS 304	:	:	:	:
Db	245 SDTYRRPGANLSTLCYASNPPAQYSWLINGTPOGSTOELFIPIITVNNSGSYTCAHNS 304	:	:	:	:
OY	305 DTGNARTTVTTITYAAP--KPFITSNNSNPVEDDAVALCEPEIQWYYIAMVWNQ 361	:	:	:	:
Db	305 VTGNCRRTVKTIITELSPVAKFKIASKTITVTGDSDVNLCTSTDGTGISLRWFKNQ 364	:	:	:	:
OY	362 SLPVSPRLQLSNDNRITLLSVTRNDVGPEECGIQNELSDVHSDPVLANTLYG--PDDPT 419	:	:	:	:
Db	365 SLPSSEBMKLQSQTITSLINPVAREBDGTWCVFNPDISKQNSDPTMLANNVNALPDENG 424	:	:	:	:
OY	420 ISP 422	:	:	:	:
Db	425 LSP 427	:	:	:	:

RESULT 8

QSR9N6_PONPY
AC QSR9N6; PRT; 525 AA.

DT 01-FEB-2005 (TrEMBLrel_29, Created)

DT 01-FEB-2005 (TrEMBLrel_29, Last sequence update)

DT 01-FEB-2005 (TrEMBLrel_29, Last annotation update)

D5 Hypothetical protein DKFZp469J1620;

D6 Name=DKFZp469J1620;

OS Pongo pygmaeus (Orangutan).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;

CK Pongo.

NC NCB1_FaxID=9600;

RN NUCLEOTIDE SEQUENCE.

RP TISSUE=kidney;

RG The German cDNA Consortium;

RA Bleicher H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,
Osanger A., Fobo G., Han M., Wiemann S.;
Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.

FL EMBL; CR6893350; CAH91524.1; -, mRNA.

DR InterPro; IPR000276; GPCR_Rhodopn.

DR InterPro; IPR003599; IG.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003598; IG_c2.

DR Pfam; PF00047; Ig; 3.

DR SMART; SM00409; Ig; 4.

DR SMART; SM00408; IGC2; 3.

DR PROSITE; PS00237; G PROTEIN RECP_FL_1; UNKNOWN_1.

KR PROSITE; PSS0835; IG LIKE; 3.

DR Hypothetical protein; Immunoglobulin domain.

SO SEQUENCE 525 AA; 57728 MW; 32BED1597026EEA3 CRC64;

Query Match 41.0%; Score 1526.5; DB 2; Length 525;

RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahy J., Helton B., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA	Scherer A., Schön J.E., Jones S.J.M., Marra M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences,"
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN	[4]
RP	PROTEIN SEQUENCE OF 35-49.
RX	PubMed:15340161; DOI:10.1101/ps.04682504;
RA	Zhang Z., Henzel W.J.,
RT	"Signal peptide prediction based on analysis of experimentally
RT	verified cleavage sites."
RL	Protein Sci. 13:2819-2824 (2004).
CC	- I - SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC	- I - SIMILARITY: Belongs to the immunoglobulin superfamily. CEA family.
CC	- I - SIMILARITY: Contains 2 Ig-like C2-type (immunoglobulin-like)
CC	domains.
CC	- I - SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like)
CC	domain.

CC	This Swiss-Prot entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use as long as its content is in no way modified and this statement is not
CC	removed.
CC	
DR	EMBL, M29541; AAA59915.1; -; mRNA.
DR	EMBL, M18728; AAAS9907.1; -; mRNA.
DR	HSSP, BC005008; AAH05008.1; -; mRNA.
DR	HSSP, Q61353; I16Z.
DR	Ensembl: ENSG0000086548; Homo sapiens.
DR	HGNc: HGNC:1818; CEACAM6.
DR	H-InVDB: HIX0015160; --.
DR	MIM, 163980; --.
DR	GO: GO:0005887; C:integral to plasma membrane; TAS.
DR	GO: GO:0007267; P:cell-cell signaling; TAS.
DR	GO: GO:0007165; P:signal transduction; TAS.
DR	InterPro: IPRO07110; Ig-like.
DR	InterPro: IPRO03598; Ig_c2.
DR	Pfam, PF00047; Ig_2.
DR	SMART, SM00408; IGc2; 1.
DR	PROSITE, PS50835; IG LIKE; 2.
KW	Antigen; Direct protein sequencing; Glycoprotein; GPI-anchor;
KW	Immunoglobulin domain; Lipoprotein; Membrane; Repeat; Signal.
FT	SIGNAL
FT	1
FT	34
FT	CHAIN
FT	35
FT	320
FT	PROPEP
FT	321
FT	344
FT	DOMAIN
FT	35
FT	142
FT	145
FT	232
FT	DOMAIN
FT	237
FT	314
FT	LIPID
FT	320
FT	310
FT	CARBOHYD
FT	104
FT	104
FT	CARBOHYD
FT	111
FT	111
FT	CARBOHYD
FT	115
FT	115
FT	CARBOHYD
FT	152
FT	152
FT	CARBOHYD
FT	173
FT	173
FT	CARBOHYD
FT	197
FT	197
FT	CARBOHYD
FT	224
FT	224
FT	CARBOHYD
FT	256
FT	256
FT	CARBOHYD
FT	274
FT	274
FT	CARBOHYD
FT	288
FT	288
FT	CARBOHYD
FT	292
FT	292
FT	CARBOHYD
FT	309
FT	309
FT	DISULFID
FT	167
FT	215
FT	DISULFID
FT	259
FT	CONFLICT
FT	138
FT	138
FT	CONFLICT
FT	239
FT	239

SEQ	SEQUENCE	344 AA;	37237 MW;	4322C5D6E25849F5 CRC64;
Query Match		38.8%;	Score 1443;	DB 1; Length 344;
Best Local Similarity		83.9%;	Pred. No. 1.9e-74;	
Matches	271;	Conservative 11;	Mismatches 41;	Indels 0; Gaps 0;
QY	1 MESSAPAPRHCITPWORLLLTASLLTFNNPPTAKLTIESIPFVNAEKEVLLVHNLPQ	60		
DB	1 MGPPSAPPCRLHVPWKEVLLTASLLTFNNPPTAKLTIESIPFVNAEKEVLLVHNLPQ	60		
QY	61 HLFQSWYKGERVQGNROIIGYVIGTQOATPGPAGSGRETIYPNASSLLIONIDTGFY	120		
DB	61 NRIQSWYKGERVQGNLSIVYVIGTQOATPGPAGSGRETIYPNASSLLIONIDTGFY	120		
QY	121 TLHAVIKSDLVNEAATGQFRVYPPELPKPSISSNNKSPVEDKDAVAFTCEPETODAITYLMWV	180		
DB	121 TLQVTKSDLVNEAATGQPHVYPPELPKPSISSNNNPVEDKDAVAFTCEPETQNTITYLMWV	180		
QY	181 NNGSLPVPSPRLQLSNGNKTLLTFENVTRNDTASYCEFTQNPVSAKSDSVILNLYGPDAP	240		
DB	181 NNGSLPVPSPRLQLSNGNKTLLTFENVTRNDTASYCEFTQNPVSAKSDSVILNLYGPDAP	240		
QY	241 TISPLNTSYSGEENLNSCHAASNPPOYSFNVGTQOQSGEELFINITVNNSSGYWCQ	300		
DB	241 TISSKAYNRGENLNSCHAASNPPOYSFNVGTQOQSGEELFINITVNNSSGYWCQ	300		
QY	301 AHNSDTGLNRTVTITTYVAEPP 323			
DB	301 AHNATGLNRTVTITTYVAEPP 323			
RESULT 11				
053XP7 HUMAN				
ID	053XP7 HUMAN PRELIMINARY;	PRT;	344 AA.	
AC	053XP7			
DT	13-SEP-2005 (TrEMBLrel. 31, Created)			
DT	13-SEP-2005 (TrEMBLrel. 31, Last sequence update)			
DT	13-SEP-2005 (TrEMBLrel. 31, Last annotation update)			
DB	Carcinohembryonic antigen-related cell adhesion molecule 6 (Non-specific cross reacting antigen).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	MULTIEST SEQUENCE.			
RA	Kaunine N., Chen X., Rolfe A., Hallack A., Hires L., Eisenstein S.,			
RA	Kaundanya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,			
RA	Pheasant M., Farmer A.,			
RL	Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BT009774; AAB8776.1; -; mRNA.			
DR	InterPro; IPR003599; IG.			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003598; IG_c2.			
DR	Pfam; PF00047; IG; 2.			
DR	SMART; SM00408; IG; 3.			
DR	SMART; SM00409; IGC; 2.			
DR	PROSITE; PSS0835; IG-LIKE; 2.			
KW	Immunoglobulin domain.			
SQ	SEQUENCE 344 AA; 37237 MW; 4322C5D6E25849F5 CRC64;			
Query Match		38.8%;	Score 1443;	DB 2; Length 344;
Best Local Similarity		83.9%;	Pred. No. 1.9e-74;	
Matches	271;	Conservative 11;	Mismatches 41;	Indels 0; Gaps 0;
QY	1 MESSAPAPRHCITPWORLLLTASLLTFNNPPTAKLTIESIPFVNAEKEVLLVHNLPQ	60		
DB	1 MGPPSAPPCRLHVPWKEVLLTASLLTFNNPPTAKLTIESIPFVNAEKEVLLVHNLPQ	60		
QY	61 HLFQSWYKGERVQGNROIIGYVIGTQOATPGPAGSGRETIYPNASSLLIONIDTGFY	120		
DB	61 NRIQSWYKGERVQGNLSIVYVIGTQOATPGPAGSGRETIYPNASSLLIONIDTGFY	120		
QY	121 TLHAVIKSDLVNEAATGQFRVYPPELPKPSISSNNKSPVEDKDAVAFTCEPETODAITYLMWV	180		
DB	121 TLQVTKSDLVNEAATGQPHVYPPELPKPSISSNNNPVEDKDAVAFTCEPETQNTITYLMWV	180		
QY	181 NNGSLPVPSPRLQLSNGNKTLLTFENVTRNDTASYCEFTQNPVSAKSDSVILNLYGPDAP	240		
DB	181 NNGSLPVPSPRLQLSNGNKTLLTFENVTRNDTASYCEFTQNPVSAKSDSVILNLYGPDAP	240		
QY	241 TISPLNTSYSGEENLNSCHAASNPPOYSFNVGTQOQSGEELFINITVNNSSGYWCQ	300		
DB	241 TISSKAYNRGENLNSCHAASNPPOYSFNVGTQOQSGEELFINITVNNSSGYWCQ	300		
QY	301 AHNSDTGLNRTVTITTYVAEPP 323			
DB	301 AHNATGLNRTVTITTYVAEPP 323			

```
QY 121 TLHVIKSDLVNEBATQGFVRYPELPKPSISISNNKSPVEDKDAVAFTCEPETODATYLMWV 180
DB 121 TLQVIKSDLVNEBATQGFHYVPELPKPSISISNNKSPVEDKDAVAFTCEPEVONTYLLMWV 180
QY 181 NNQSLPVSFPRQLQSLNGNRTLLTFNVTNRDNTASYKCETONPVSARSDSVILNVLYGPDAP 240
DB 181 NNQSLPVSFPRQLQSLNGNMTLLTSVKRNDAGSYECEIQNPASANRSDPVTLLNVLYGPDAP 240
QY 241 TISPLNTSYRSGENLNLSCHAASNPPAOYSWPNNGFPOOSTOELFIPNITVNNSSGYTQ 300
DB 241 TISPSKANRPGENLNLSCHAASNPPAOYSWPNNGFPOOSTOELFIPNITVNNSSGYTQ 300
QY 301 AHNSDTGLNRTTITVTITVYAEPP 323
DB 301 AHN SATGLNRTTITVTITVSGSNP 323

RESULT 12
Q13774 HUMAN PRELIMINARY; PRT; 344 AA.
ID Q13774
AC Q13774
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE NCA protein precursor.
GN Name=NCA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OC NCBI_TaxID=9606;
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=88139389; PubMed=2830274;
RA Neumaier M., Zimmermann W., Shively L., Hinoda Y., Riggs A.D.,
RA Shively J.E.;
RT "Characterization of a cDNA clone for the nonspecific cross-reacting
RT antigen (NCA) and a comparison of NCA and carcinoembryonic antigen,"
RL J. Biol. Chem. 263:3202-3207(1988).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=87298464; PubMed=3618991;
RA Oikawa S., Kosaki G., Nakazato H.;
RT "Molecular cloning of a gene for a member of carcinoembryonic antigen
RT (CEA) gene family: signal peptide and N-terminal domain sequences of
RT nonspecific crossreacting antigen (NCA).",
RC Biochem. Biophys. Res. Commun. 146:464-469(1987).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).
DR EMBL; M18216; AAA51739.1; -; mRNA.
DR PIR; A26902; A27681.
DR HSSP; O61353; 1162.
DR Ensembl; ENSG00000086548; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00408; IgC2; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
KW Immunoglobulin domain; Signal; Transmembrane.
FT SIGNAL 1
FT CHAIN 35 344 Potential.
SQ SEQUENCE 344 AA; 37195 MW; 28469487A74C18A4 CRC64;

Query Match 38.8%; Score 1443; DB 2; Length 344;
Best local Similarity 83.9%; Pred. No. 1.9e-74;
Matches 271; Conservative 11; Mismatches 41; Indels 0; Gaps 0;

QY 1 MESPSAPPHRMCIIPWRLITLTLTFMNPPTAKLTISTEPNVAEGKEVLLVHNLPO 60
DB 1 MGPPSAPPCRLIHPWKEVLLTSLTFMNPPTAKLTISTEPNVAEGKEVLLVHNLPO 60
QY 61 HLFGRYWKGERVDGNROITIGYITGOATPGAYSGRETIYNASLLIIONITQNDTGRY 120
DB 61 HLFGRYWKGERVDGNROITIGYITGOATPGAYSGRETIYNASLLIIONITQNDTGRY 120
```

```
DB 61 NRIGYSWKGERVDGNSLIVGYICTGOATPGPAYSGRETIYNASLLIIONITQNDTGRY 120
QY 121 TLHVIKSDLVNEBATQGFVRYPELPKPSISISNNKSPVEDKDAVAFTCEPETODATYLMWV 180
DB 121 TLQVIKSDLVNEBATQGFHYVPELPKPSISISNNKSPVEDKDAVAFTCEPEVONTYLLMWV 180
QY 181 NNQSLPVSFPRQLQSLNGNRTLLTFNVTNRDNTASYKCETONPVSARSDSVILNVLYGPDAP 240
DB 181 NNQSLPVSFPRQLQSLNGNMTLLTSVKRNDAGSYECEIQNPASANRSDPVTLLNVLYGPDAP 240
QY 241 TISPLNTSYRSGENLNLSCHAASNPPAOYSWPNNGFPOOSTOELFIPNITVNNSSGYTQ 300
DB 241 TISPSKANRPGENLNLSCHAASNPPAOYSWPNNGFPOOSTOELFIPNITVNNSSGYTQ 300
QY 301 AHNSDTGLNRTTITVTITVYAEPP 323
DB 301 AHN SATGLNRTTITVTITVSGSNP 323

RESULT 13
Q5UB49 HUMAN PRELIMINARY; PRT; 368 AA.
ID Q5UB49
AC Q5UB49
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Putative carcinoembryonic antigen-related cell adhesion molecule 1
DE short form 3.
GN Name=CEACAM1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OC NCBI_TaxID=9606;
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Long S., Phillips A., Ma H., Paoni N.F., Wong-Staal F., Fan W.;
RT "Isolation of the cDNA encoding a putative carcinoembryonic antigen-
RT related cell adhesion molecule 1 short form 3 (CEACAM1-3S).",
RL Submitted (SEP-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY766113; AAJ34600.1; -; mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR000920; Myelin_P0.
DR Pfam; PF00047; Ig_2.
DR PRINTS; PR00213; MYELINPO.
DR SMART; SM00409; IG_3.
DR SMART; SM00408; IgC2; 2.
DR PROSITE; PS00237; G_PROTEIN_RECPT_P1_1; UNKNOWN_1.
KW Immunoglobulin domain.
SQ SEQUENCE 368 AA; 39871 MW; 23D7E54B4DC54318 CRC64;

Query Match 38.3%; Score 1426.5; DB 2; Length 368;
Best local Similarity 76.7%; Pred. No. 1.8e-73;
Matches 276; Conservative 16; Mismatches 39; Indels 29; Gaps 2;

QY 5 SAPPHRMCIIPWRLITLTLTFMNPPTAKLTISTEPNVAEGKEVLLVHNLPOHLFG 64
DB 5 SAPLHRVWPQGLLTLTLTFMNPPTAQLTTSMPNVAEGKEVLLVHNLPOQLFG 64
QY 65 YSMYKGERVDGNROITIGYITGOATPGAYSGRETIYNASLLIIONITQNDTGRYTLHV 124
DB 65 YSMYKGERVDGNROITIGYITGOATPGAYSGRETIYNASLLIIONITQNDTGRYTLQV 124
QY 125 IKSDDLVEBATQGFVRYPELPKPSISISNNKSPVEDKDAVAFTCEPETODATYLMWVNNQS 184
DB 125 IKSDDLVEBATQGFHYVPELPKPSISISNNKSPVEDKDAVAFTCEPETODATYLLMWVNNQS 184
QY 185 LPSFPRQLQSLNGNRTLLTFNVTNRDNTASYKCETONPVSARSDSVILNVLYGPDAPFTSP 244
DB 185 LPSFPRQLQSLNGNRTLLTFNVTNRDNTASYKCETONPVSARSDSVILNVLYGPDAPFTSP 244
```

```

Db      185 LPSVRLQLSNGNRTLLTSLVTRNDTGPYECETQNPVSNRSDPVTIANVTPDPPTISP 244
Qy      245 LNTSYRSGENLNLSCHAASNPPAOYSWFGNGFOOSTOELFIPNITVNNSGSYTCOAHNS 304
Db      245 SYTYRPGANLSLSCYAASNPPAOYSWFLNGFOOSTOELFIPNITVNNSGSYTCOAHNS 304
Qy      305 DTGLNRTVTVTITVVAEPPKPFITSNNSNPVEDE-----DAVALTLC 345
Db      305 VTGCNRTVTKITI-----ITVDNALPQENGLSPGALAGIVIGVALVALIIVALAC 354

RESULT 14
ID      013854 HUMAN PRELIMINARY; PRT; 461 AA.
AC      013854;
DT      01-NOV-1996 (TREMBLrel. 01, Created)
DT      01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT      01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE      Biliary glycoprotein.
GN      Name=BGP;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC      Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RA      MEDLINE=89139550; PubMed=2537311; DOI=10.1083/jcb.108.2.267;
RA      Barnett T.R., Kretschmer A., Austen D.A., Goebel S.J., Hart J.T.,
RA      Elting J.J., Kamarek M.E.;
RT      "Carcinoembryonic antigens: alternative splicing accounts for the
RT      multiple mRNAs that code for novel members of the carcinoembryonic
RT      antigen family.";
RL      J. Cell Biol. 108:267-276 (1989).
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RA      Kuroki M., Matsuo Y., Mismuni Y., Oikawa S., Matsuo Y.;
RA      Submitted (JUN-1992) to the EMBL/GenBank/DBJ databases.
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
DR      EMBL; D12502; BAA02063.1; -, mRNA.
DR      HSP; Q61353; I16Z.
DR      Ensemble; ENSG00000079385; Homo sapiens.
DR      InterPro; IPR000276; GPCR_Rhodopsn.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003598; Ig_c2.
DR      Pfam; PF00047; Ig_2.
DR      SMART; SM00408; IgC2; 1.
DR      PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR      PROSITE; PS50835; IG_LIKE; 2.
KW      Immunoglobulin domain.
SQ      SEQUENCE 461 AA; 50298 MW; 4A6F0F05884C4727 CRC64;

Query Match      38.2%; Score 1423; DB 2; Length 461;
Best Local Similarity 63.0%; Pred. No. 3.9e-73;
Matches 298; Conservative 27; Mismatches 66; Indels 80; Gaps 10;

```

```

Qy      245 LNTSYRSGENLNLSCHAASNPPAOYSWFGNGFOOSTOELFIPNITVNNSGSYTCOAHNS 304
Db      245 SYTYRPGANLSLSCYAASNPPAOYSWFLNGFOOSTOELFIPNITVNNSGSYTCOAHNS 304
Qy      305 DTGLNRTVTVTITV-----YAEPPKPFIT-----SNNSNPVEDE----- 338
Db      305 VTGCNRTVTKITIYTERQNLMTLPGLDSNSNAQALPVSQSABETDVALPQENGLSPCA 364
Qy      339 -----DAVALTCEPPEIQNTTYIMVNNQSLPVSRLQLSNDNRTLLSVT 384
Db      365 IAGIVIGVALVALIIVALACFLHFGKT-----GRASDQEDLT----- 402

Qy      385 RNDVGPYCGIQNELSVDSHD--PYIIN-VLYG-----PDDPT-ISPST 425
Db      403 -----EHRPSVSNH-TQDHSNDPVMKNMEVITYSTLNFEAQOPTQPSPSLT 449

RESULT 15
ID      CEAM8 HUMAN STANDARD; PRT; 349 AA.
AC      P31997; Q60399; Q16574;
DT      01-JUL-1993 (Rel. 26, Created)
DT      15-JUL-1993 (Rel. 38, Last sequence update)
DT      10-MAY-2005 (Rel. 47, Last annotation update)
DE      Carcinoembryonic antigen-related cell adhesion molecule 8 precursor
DE      (Carcinoembryonic antigen CGM6) (Non-specific cross-reacting antigen
DE      NCA-95) (Antigen CD67) (CD66 antigen).
GN      Name=CEACAM8; Synonyms=CGM6;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC      Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      TISSUE=Spleen;
RX      MEDLINE=91003998; PubMed=2208113;
RA      Berling B., Kolbinger F., Grunert F., Thompson J.A., Brombacher F.,
RA      Buchegger F., Kleist S., Zimmermann W.;
RT      "Cloning of a carcinoembryonic antigen gene family member expressed in
RT      leukocytes of chronic myeloid leukemia patients and bone marrow.";
RL      Cancer Res. 50:6534-6539 (1990).
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RX      MEDLINE=90165902; PubMed=2306228;
RA      Arakawa F., Kuroki M., Mismuni Y., Oikawa S., Nakazato H., Matsuo Y.;
RT      "Characterization of a cDNA clone encoding a new species of the
RT      nonspecific cross-reacting antigen (NCA), a member of the CEA gene
RT      family.";
RL      Biochem. Biophys. Res. Commun. 166:1063-1071 (1990).
RN      [3]
RP      NUCLEOTIDE SEQUENCE.
RX      PubMed=1427854;
RA      Khan W.N., Fraengsmayr L., Teglund S., Israelsson A., Bremer K.,
RA      Hammarstrom S.;
RT      "Identification of three new genes and estimation of the size of the
RT      carcinoembryonic antigen family.";
RL      Genomics 14:384-390 (1992).
RN      [4]
RP      NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).
RX      PubMed=15057824; DOI=10.1038/nature02399;
RA      Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J.,
RA      Lamerdin J.E., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M.,
RA      Aerts A., Altherr M., Ashworth L., Bajorek E., Black S., Branscomb E.,
RA      Canepaee S., Carraro A.V., Caolte C., Chan Y.M., Christensen M.,
RA      Claloud C.A., Copeland A., Dalin E., Delah P., Denys M., Dexter J.C.,
RA      Escobar T., Flowers D., Fotopoulos D., Garcia C., Georgescu A.M.,
RA      Glavina T., Gomez M., Gonzales E., Groza M., Hammon N., Hawkins T.,
RA      Haydu L., Ho I., Huang W., Ibrani S., Jett J., Kadner K., Kimball H.,
RA      Kobayashi A., Laitonov V., Leem S.-H., Lopez F., Lou Y., Lowry S.,
RA      Mafaceti S., Martinez D., McCreedy P.M., Medina C., Morgan J.,
RA      Nelson K., Nolan M., Ovcharenko I., Picluc S., Pollard M.,
RA      Popkie A.P., Predki P., Quan G., Ramirez L., Rash S., Retterer J.,

```

RA Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D.,
 RA Slezak T., Solovyev V., Thayer N., Tice H., Tsai J., Ustaszewska A.,
 RA Vo N., Wagner M., Wheeler T., Wu K., Xie G., Yang J., Dubchak I.,
 RA Pury T.S., DeLong P., Dickson M., Gordon D., Richter E.E.,
 RA Pennacchio L.A., Richardson P., Stubbs L., Kohnen D.S., Myers R.M.,
 RA Rubin E.M., Lucas S.M.,
 RT "The DNA sequence and biology of human chromosome 19,"
 RT Nature 428:529-535 (2004).
 (5)
 RP NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA).
 RC TISSUE=lung;
 RX MEDLINE=23289257, PubMed=12477932, DOI=10.1073/pnas.242603899;
 RA Strusberg R.L., Reingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
 RA Diachenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.D., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Goughwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywicki M.I., Skaleka U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences,"
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 (6)
 RP NUCLEOTIDE SEQUENCE OF 1-21.
 RX MEDLINE=98102450, PubMed=9427723;
 RA Bades-Pearner A., Thompson J., van der Putten H., Zimmermann W.,
 RT "Mice transgenic for the human CGM6 gene express its product, the
 RT granulocyte marker CD66b, exclusively in granulocytes,"
 RT Blood 91:663-672 (1998).
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -1- TISSUE SPECIFICITY: Expressed in leukocytes of chronic myeloid
 CC Leukemia patients and bone marrow.
 CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily. CEA family.
 CC -1- SIMILARITY: Contains 2 Ig-like C2-type (immunoglobulin-like)
 CC domains.
 CC -1- SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like)
 CC domain.

 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

 CC EMBL, X52378; CAA3604.1; -; mRNA.
 DR EMBL, M3336; AAB59914.1; -; mRNA.
 DR EMBL, D90064; BAA14108.1; -; mRNA.
 DR EMBL, AC004558; AAC13659.1; -; Genomic_DNA.
 DR EMBL, BC026263; AAH26263.1; -; mRNA.
 DR EMBL, Z55119; CAB08296.1; -; Genomic_DNA.
 DR PIR, S13524; A34815.
 DR HSSP, Q61353; 1162.
 DR Ensembl: ENSG00000124469; Homo sapiens.
 DR HGNC, HGNC:1820; CEACAM6.
 DR H-InvDB, HIT0018406; -.
 DR MIM, 114890; -.
 DR GO, GO:0005615; C:extracellular space; TAS.
 DR GO, GO:0005887; C:integral to plasma membrane; TAS.
 DR GO, GO:0005886; C:plasma membrane; TAS.
 DR GO, GO:0006955; P:immune response; TAS.
 DR InterPro, IPR003599; Ig.
 DR InterPro, IPR007110; Ig-like.
 DR Pfam, PF00047; Ig; 1.

DR SMART, SM00409; IG; 3.
 DR PROSITE, PSS0035; IG_LIKE; 2.
 KM Antigen: Glycoprotein, GPI-anchor: Immunoglobulin domain; Lipoprotein;
 FT Membrane; Polymorphism; Repeat; Signal.
 FT SIGNAL 1 34
 FT CHAIN 35 320
 FT PROPEP 321 349
 FT DOMAIN 35 142
 FT DOMAIN 145 232
 FT DOMAIN 237 319
 FT LIPID 320 349
 FT CARBOHYD 104 104
 FT CARBOHYD 111 111
 FT CARBOHYD 115 115
 FT CARBOHYD 152 152
 FT CARBOHYD 173 173
 FT CARBOHYD 197 197
 FT CARBOHYD 224 224
 FT CARBOHYD 256 256
 FT CARBOHYD 274 274
 FT CARBOHYD 288 288
 FT CARBOHYD 309 309
 FT DISULFID 167 215
 FT DISULFID 259 299
 FT VARIANT 114 114
 FT CONFLICT 322 322
 FT SEQUENCE 349 AA; 38154 MM; AACF74DALAC839D8 CR664;
 SQ
 Query Match 34.2%; Score 1272; DB 1; Length 349;
 Best Local Similarity 76.8%; Pred. No. 1.1e-64;
 Matches 241; Conservative 19; Mismatches 54; Indels 0; Gaps 0;
 QY 5 SAPPHRMCIPWQRLITSLTFNMPPTAKTISTPPNVAEGKVLVHNLPOHLFG 64
 DB 5 SAPSCRMRLPWQGLITSLTFNMPPTAQLTIAVPSNAEGKVELLVHNLPODERG 64
 QY 65 YSMYGERVDGKROIIIGVIGTQOATPGPAYSGREIYNASLLIIONITONTGFTLHV 124
 DB 65 YMYKGETVDANKRIIIGVISMQITPPPAYSNRETIYNASLLMRNVRNDTSGTLOY 124
 QY 125 IKSDEVNEBATQFRVPELPKPSISNNKSEVEDKDAVAFTCEPETODATYLMWVNGS 184
 DB 125 IKLNLMSSEVTQOFVHPETPKPSISNNNSNVEDKDAVAFCEPETQVITYLWVNGS 184
 QY 185 LVSYPRLQSNNGRITLTLENVTRNDTASAKGETQNPVSRKSDSYLVNLVYEPDAPTISP 244
 DB 185 LVSYPRLQSNNGRITLTLENVTRNDVGPYECBIQNPASANFSDPVTLNLVYGPDAPTISP 244
 QY 245 LNTSVKSGENLMLSGHAASNPAPQXSWFVNGTFOOSTOELFIPNITVNNSGSYTCQAHNS 304
 DB 245 SPTVYHAGVNLMLSGHAASNPSPQYSWVNGTFOOYTQQLFIPNITTKSGSYACTHTNS 304
 QY 305 DTGLNRTVYTTITV 318
 DB 305 ATGRNRTVYTTITV 318
 Search completed: April 10, 2006, 18:06:36
 Job time : 239.861 secs

OM protein - protein search, using sw model

Run on: April 10, 2006, 17:55:05 ; Search time 270.297 Seconds

1141.129 Million cell updates/sec

Title: US-10-734-564-72

Sequence: 1 MESPSAPPHRWCIWQRL...LSAGATVGMIGLVGVALI 702

Scoring table: BLOSUM62

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_21:*

A_Geneseq_21.*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3721	100.0	702	5	ABU75931	ABU75931 Carcinogen
2	3721	100.0	702	5	ABU56667	ABU56667 Lung cancer
3	3721	100.0	702	6	ABU56426	ABU56426 Lung cancer
4	3721	100.0	702	6	ADAB84059	ADAB84059 Human CBR
5	3721	100.0	702	6	ABP74707	ABP74707 Human CBR
6	3721	100.0	702	6	ABU04837	ABU04837 Human exp
7	3721	100.0	702	6	ABU04800	ABU04800 Human exp
8	3721	100.0	702	6	ABU04834	ABU04834 Human exp
9	3721	100.0	702	6	ABU04796	ABU04796 Human exp
10	3721	100.0	702	7	ABR82476	ABR82476 Human car
11	3721	100.0	702	7	ADC09591	ADC09591 CBR prote
12	3721	100.0	702	7	ADD25526	ADD25526 Binding c
13	3721	100.0	702	7	ADD46175	ADD46175 Human p
14	3721	100.0	702	7	ADD84721	ADD84721 Human car
15	3721	100.0	702	7	ADN39014	ADN39014 Cancer/an
16	3721	100.0	702	8	ADM72829	ADM72829 Human CBR
17	3721	100.0	702	8	ADO49153	ADO49153 Human car
18	3721	100.0	702	8	ADO28645	ADO28645 Human CBR
19	3721	100.0	702	8	ADQ29646	ADQ29646 Human car
20	3721	100.0	702	8	ADP80107	ADP80107 Human exp
21	3721	100.0	702	8	ADT50889	ADT50889 Cancer re
22	3721	100.0	702	8	ADT77676	ADT77676 Human car
23	3721	100.0	702	8	ADU06621	ADU06621 Human b
24	3721	100.0	702	8	ADUV3922	ADUV3922 Human car

25	3721	100.0	702	9	ADV73224	Human	col
26	3721	100.0	702	9	ADV73228	Human	col
27	3721	100.0	702	9	ABR29747	Human	car
28	3721	100.0	708	8	ADR89125	Human	car
29	3721	100.0	734	2	AAW00182	Human	car
30	3721	100.0	734	6	ABU04823	Carcinom	
31	3718	99.9	796	4	ABF70880	Human	exp
32	3718	99.9	796	6	ABU04812	Human	car
33	3714	99.8	702	8	ADO38542	Human	exp
34	3713	99.8	702	8	ADM12332	Carcinom	
35	3710.5	99.7	703	8	ADU04913	Human	car
36	3701.5	99.5	701	4	ABR97817	Carcinom	
37	3701.5	99.5	701	4	AAE05117	Modified	
38	3701.5	99.5	701	5	AAE05117	Modified	
39	3700	99.4	698	2	AAE7918	CEA agnol	
40	3700	99.4	698	2	AAE65168	Carcinom	
41	3700	99.4	698	2	AAW22844	Carcinom	
42	3700	99.4	698	6	ABU04822	Human	car
43	3700	99.4	698	6	ABU04806	Human	exp
44	3700	99.4	698	6	ABU04798	Human	exp
45	3694	99.3	702	1	ABU04827	Human	exp
					AAE94014	Carcinom	

ALIGNMENTS

RESULT 1	
ABB75931	
ID	ABB75931 standard; protein; 702 AA.
XX	
AC	ABB75931;
XX	
DT	01-JUL-2002 (first entry)
XX	
DE	Carcinoembryonic antigen.
XX	
KM	Carcinoembryonic antigen; CEA; epitope; human leucocyte antigen; HLA;
KW	major histocompatibility complex; MHC; CD4; T lymphocyte; cancer; tumour
KX	cytostatic; antitumour; therapy; diagnosis; human; human.
OS	Homo sapiens.
XX	
PN	WO200222803-A2.
XX	
PD	21-MAR-2002.
XX	
PF	12-SEP-2001; 2001WO-US028467.
XX	
PR	12-SEP-2000; 2000US-0232185P.
XX	
PA	(ZYCO-) ZYCO5 INC.
XX	
PI	Chicz R, Tomlinson A;
XX	
DR	WPI; 2002-362345/39.
DR	N-PSDB; ABL54023.
XX	
PT	Identifying human leukocyte antigen (HLA) class II-restricted epitopes,
CC	comprises isolating a major histocompatibility complex (MHC) molecule
PT	bound to a peptide and eluting the peptide.
XX	
PS	Example 1; Fig 1B; 98pp; English.
XX	
CC	The present sequence is the protein sequence for human carcinoembryonic
CC	antigen (CEA). Epstein-Barr virus-transformed B cell lines expressing CEA
CC	encoding cDNA were used to identify human leukocyte antigen (HLA) Class
CC	II binding CEA peptide epitopes. The invention provides methods for
CC	identifying peptide epitopes that activate CD4+ T lymphocyte responses
CC	involved in the initiation, promotion, or exacerbation of certain
CC	diseases. It is based on the discovery that it is possible to identify
CC	human leukocyte antigen class II restricted epitopes naturally produced
CC	by antigen-presenting cells transfected with DNA encoding a protein from
CC	which the epitopes are derived. The method has 2 phases: immunological

CC mass fingerprinting, and epitope verification. By applying the methods to
CC the tumour antigen CEA, CEA-derived peptides (see AB875917-26) were
CC identified as epitopes that could be involved in the pathogenesis of
CC cancer in human patients expressing the DR4 or DR1 class II major
CC histocompatibility complex (MHC) allele. The epitopes of, and altered
CC peptide ligands (APL), are used in claimed methods of activating T cell
CC reactivity, altering T cell response, diagnosis, and identifying a
CC reagent for diagnosing cancer. Also claimed are methods of cancer
CC therapy, and of identifying a class II MHC-binding fragment of a tumour
CC antigen. APLs are also useful as vaccines

XX
SQ Sequence 702 AA;

Query Match 100.0%; Score 3721; DB 5; Length 702;

Best Local Similarity 100.0%; Pred. No. 1.4e-199; Indels 0; Gaps 0;

Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSPAPPHRWCTPWQRLLLTASLTFNNPPTAKLTISTPPNVAEGKVVLLVNNLPQ 60
DB 1 MESSPAPPHRWCTPWQRLLLTASLTFNNPPTAKLTISTPPNVAEGKVVLLVNNLPQ 60
QY 61 HLFPGYSWYGERVDGNRQIIIGYIGTQATPGPAGSGRETIYPNASLLIQNIITQNDTGFY 120
DB 61 HLFPGYSWYGERVDGNRQIIIGYIGTQATPGPAGSGRETIYPNASLLIQNIITQNDTGFY 120
QY 121 TLHVIKSDLVNEBATGQFRVYPELPKPSISSNNKSPVEDKDAVAFCEPETODATYLMWV 180
DB 121 TLHVIKSDLVNEBATGQFRVYPELPKPSISSNNKSPVEDKDAVAFCEPETODATYLMWV 180
QY 181 NNQSLPVSRLQISNGNRLLTFNNTRNDTASYKCTQNPVSARRSDSVILNLYGPDAP 240
DB 181 NNQSLPVSRLQISNGNRLLTFNNTRNDTASYKCTQNPVSARRSDSVILNLYGPDAP 240
QY 241 TISPLNTSYRSGENLNLSCHAASNPPAOYSWPNFGFOOSTOGLFIPNITVNNSSGYTQ 300
DB 241 TISPLNTSYRSGENLNLSCHAASNPPAOYSWPNFGFOOSTOGLFIPNITVNNSSGYTQ 300
QY 301 AANSDTGLNRTTYTTTVAEPKPPITSNNSNPVEDKDAVATCEPEIQNTTYLMMVNN 360
DB 301 AANSDTGLNRTTYTTTVAEPKPPITSNNSNPVEDKDAVATCEPEIQNTTYLMMVNN 360
QY 361 QSLPVSRLQISNDNRLLTLLSVTRNDVGYEBCGIONELSVHSDPVIILNLYGPDPTI 420
DB 361 QSLPVSRLQISNDNRLLTLLSVTRNDVGYEBCGIONELSVHSDPVIILNLYGPDPTI 420
QY 421 SPSYTYRRGVNLISLSCHAASNPPAOYSWLIIDENIQOHTQELFISNITEKNSGLYTCQAN 480
DB 421 SPSYTYRRGVNLISLSCHAASNPPAOYSWLIIDENIQOHTQELFISNITEKNSGLYTCQAN 480
QY 481 NSASGHSRTTVAETIVSAELPKPSISSNNKSPVEDKDAVAFCEPEAQNTTYLMMVNGOS 540
DB 481 NSASGHSRTTVAETIVSAELPKPSISSNNKSPVEDKDAVAFCEPEAQNTTYLMMVNGOS 540
QY 541 LFPVSRLQISNGNRLLTFNNTRNDARAAYCGIQNSVANSRSDPVLTVLGYGDPDIIS 600
DB 541 LFPVSRLQISNGNRLLTFNNTRNDARAAYCGIQNSVANSRSDPVLTVLGYGDPDIIS 600
QY 601 PSSSYLGGANLNLSCHASNPPOYSWRINGIPQOHTQVLFIKITPNNNGTACFVSNN 660
DB 601 PSSSYLGGANLNLSCHASNPPOYSWRINGIPQOHTQVLFIKITPNNNGTACFVSNN 660
QY 661 ATGRNNSIVKSIIVSASGTSPLSAGATVGMIGVAVGVALI 702
DB 661 ATGRNNSIVKSIIVSASGTSPLSAGATVGMIGVAVGVALI 702

RESULT 2
ABUS6667
ID ABUS6667 standard; protein; 702 AA.
XX
AC ABUS6667;
XX
DT 02-APR-2003 (first entry)

XX
DE Lung cancer-associated polypeptide #260.

XX Lung cancer-associated polypeptide; cytostatic; emphysema;
XX antiinflammatory; antineoplastic; non-small cell lung cancer; atelectasis;
XX small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
XX chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
XX interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

XX Unidentified.

XX WO2002086443-A2.

XX 31-OCT-2002.

XX 18-APR-2002; 2002WO-US012476.

XX 18-APR-2001; 2001US-0284770P.

XX 10-MAY-2001; 2001US-0290492P.

XX 09-NOV-2001; 2001US-0339245P.

XX 13-NOV-2001; 2001US-0350666P.

XX 29-NOV-2001; 2001US-0334370P.

XX 12-APR-2002; 2002US-0372246P.

XX (EOSB-) EOS BIOTECHNOLOGY INC.

XX Aziz N, Murray R;

XX WPI, 2003-093161/08.

XX N-PSDB; ABX76396.

XX Detecting a lung cancer-associated transcript in a cell from a patient

XX for treating lung cancer, by contacting a biological sample from the

XX patient with a polynucleotide that exhibits increased or decreased

XX expression in lung cancer.

XX Claim 27; Page 390; 453pp; English.

XX The invention relates to a method for detecting a lung cancer-associated
XX transcript in a cell from a patient, comprising contacting a biological
XX sample from the patient with a polynucleotide that selectively hybridizes
XX to a sequence that is at least 80 % identical to a gene that exhibits
XX increased or decreased expression in lung cancer samples. Lung cancer-
XX associated polynucleotides and polypeptides are used for identifying a
XX compound that modulates a lung cancer-associated polypeptide, for
XX inhibiting proliferation of a lung cancer-associated cell to treat lung
XX cancer in a patient and for treating a mammal having lung cancer by
XX administering a modulatory compound identified. The methods are useful
XX for treating lung cancer, such as small cell lung cancer, non-small cell
XX lung cancer or other benign or precancerous lesions, e.g. atelectasis,
XX emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
XX hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
XX bronchiectasis. The genes, polynucleotides and polypeptides are useful
XX for diagnostic purposes and as targets for screening for therapeutic
XX compounds that modulate lung cancer, such as antibodies. Sequences
XX ABUS6408-ABUS6745 represent lung cancer-associated polypeptides of the
XX invention

XX
SQ Sequence 702 AA;

Query Match 100.0%; Score 3721; DB 6; Length 702;

Best Local Similarity 100.0%; Pred. No. 1.4e-199; Indels 0; Gaps 0;

Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSPAPPHRWCTPWQRLLLTASLTFNNPPTAKLTISTPPNVAEGKVVLLVNNLPQ 60

DB 1 MESSPAPPHRWCTPWQRLLLTASLTFNNPPTAKLTISTPPNVAEGKVVLLVNNLPQ 60

QY 61 HLFPGYSWYGERVDGNRQIIIGYIGTQATPGPAGSGRETIYPNASLLIQNIITQNDTGFY 120

DB 61 HLFPGYSWYGERVDGNRQIIIGYIGTQATPGPAGSGRETIYPNASLLIQNIITQNDTGFY 120

QY 121 TLHVIKSDLVNEBATGQFRVYPELPKPSISSNNKSPVEDKDAVAFCEPETODATYLMWV 180

Db 121 TLHVYKSDLVNEAATGQFRVYDELPRKPSISSNNSKPVEDKDAVAFTCEPETQDATYLMWV 180
Qy 181 NNQSLPVSPRLQLSNGNRTLTLFNTTRNDTASYKETONPVARSDSVILNLYGPDAP 240
Db 181 NNQSLPVSPRLQLSNGNRTLTLFNTTRNDTASYKETONPVARSDSVILNLYGPDAP 240
Qy 241 TISPLNTSYRSGENLNSCHAAASNPAPQYSWFVNGTFOOSTOELFIPNTVNNSSSYTCQ 300
Db 241 TISPLNTSYRSGENLNSCHAAASNPAPQYSWFVNGTFOOSTOELFIPNTVNNSSSYTCQ 300
Qy 301 AHNSDTGLNRTTNTTITVYAEPPKPFITSNNSNPVEDDAVALTCEPEIQNTTYLWVNN 360
Db 301 AHNSDTGLNRTTNTTITVYAEPPKPFITSNNSNPVEDDAVALTCEPEIQNTTYLWVNN 360
Qy 361 QSLPVSPRLQLSNDNRRTLTLSTVRNDVGPYECGIONELSDHSDPVILNLYGPDPTI 420
Db 361 QSLPVSPRLQLSNDNRRTLTLSTVRNDVGPYECGIONELSDHSDPVILNLYGPDPTI 420
Qy 421 SPSYTYRPGVNLISCHAAASNPAPQYSWMLIDGNIQOHTOELFISNTEKNSGLYTCQAN 480
Db 421 SPSYTYRPGVNLISCHAAASNPAPQYSWMLIDGNIQOHTOELFISNTEKNSGLYTCQAN 480
Qy 481 NSASGHSRTTYKTIIVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWVNGQS 540
Db 481 NSASGHSRTTYKTIIVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWVNGQS 540
Qy 541 LPVSPRLQLSNGNRTLTLFNTTRNDARAAYVCIGIONSVSANSRDPYTLNLYGPDPTI 600
Db 541 LPVSPRLQLSNGNRTLTLFNTTRNDARAAYVCIGIONSVSANSRDPYTLNLYGPDPTI 600
Qy 601 PDSSYLSGANLNSCHASNPSPPOYSWRLNGIPQOHTOELFIPNTVNNNGTYACFVSNL 660
Db 601 PDSSYLSGANLNSCHASNPSPPOYSWRLNGIPQOHTOELFIPNTVNNNGTYACFVSNL 660
Qy 661 ATGRNNSIVKSIIVSASGTSQGLSAGATVGMIGVLVGVALI 702
Db 661 ATGRNNSIVKSIIVSASGTSQGLSAGATVGMIGVLVGVALI 702

RESULT 3
ABUS6426
ID ABUS6426 standard; protein; 702 AA.
XX
AC ABUS6426;
XX
DT 02-APR-2003 (first entry)
XX
DE Lung cancer-associated polypeptide #19.
XX
KW Lung cancer-associated polypeptide; cytostatic; emphysema;
KW antiinflammatory; antisthmatic; non-small cell lung cancer; atelectasis;
KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX
OS unidentified.
XX
PN WO200286443-A2.
XX
PD 31-OCT-2002.
XX
PF 18-APR-2002; 2002WO-US012476.
XX
PR 18-APR-2001; 2001US-0284770P.
XX
PR 10-MAY-2001; 2001US-0290492P.
XX
PR 09-NOV-2001; 2001US-0339245P.
XX
PR 13-NOV-2001; 2001US-0350666P.
XX
PR 29-NOV-2001; 2001US-0334370P.
XX
PR 12-APR-2002; 2002US-0372246P.
XX
PA (BOSB-) EOS BIOTECHNOLOGY INC.

PI Aziz N, Murray R;
XX
XX MPI: 2003-093161/08.
DR N-PSDB; ABX76144.
XX
XX
PT Detecting a lung cancer-associated transcript in a cell from a patient
PT for treating lung cancer, by contacting a biological sample from the
PT patient with a polynucleotide that exhibits increased or decreased
PT expression in lung cancer.
XX
PS Claim 27; Page 204; 453p; English.
XX
XX
XX The invention relates to a method for detecting a lung cancer-associated
XX transcript in a cell from a patient, comprising contacting a biological
XX sample from the patient with a polynucleotide that selectively hybridizes
XX to a sequence that is at least 80 % identical to a gene that exhibits
XX increased or decreased expression in lung cancer samples. Lung cancer-
XX associated polynucleotides and polypeptides are used for identifying a
XX compound that modulates a lung cancer-associated polypeptide, for
XX inhibiting proliferation of a lung cancer-associated cell to treat lung
XX cancer in a patient and for treating a mammal having lung cancer by
XX administering a modulatory compound identified. The methods are useful
XX for treating lung cancer, such as small cell lung cancer, non-small cell
XX lung cancer or other benign or precancerous lesions, e.g. atelectasis,
XX emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
XX hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
XX bronchiectasis. The genes, polynucleotides and polypeptides are useful
XX for diagnostic purposes and as targets for screening for therapeutic
XX compounds that modulate lung cancer, such as antibodies. Sequences
XX ABUS6408-ABUS6745 represent lung cancer-associated polypeptides of the
XX invention
SQ Sequence 702 AA;
Query Match 100.0%; Score 3721; DB 6; Length 702;
Best Local Similarity 100.0%; Pred. No. 1,4e-199;
Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MESBPAPHRKCIPIQRLTLTASLTTFWNPPTAKLTIESPPNVAEGKEVILLVHNTLPQ 60
Db 1 MESBPAPHRKCIPIQRLTLTASLTTFWNPPTAKLTIESPPNVAEGKEVILLVHNTLPQ 60
Qy 61 HLFQSWYKGRVQGNROIIGVIGTQATGPAVSGREIILYPNASSLILIONIDTGY 120
Db 61 HLFQSWYKGRVQGNROIIGVIGTQATGPAVSGREIILYPNASSLILIONIDTGY 120
Qy 121 TLHVYKSDLVNEAATGQFRVYDELPRKPSISSNNSKPVEDKDAVAFTCEPETQDATYLMWV 180
Db 121 TLHVYKSDLVNEAATGQFRVYDELPRKPSISSNNSKPVEDKDAVAFTCEPETQDATYLMWV 180
Qy 181 NNQSLPVSPRLQLSNGNRTLTLFNTTRNDTASYKETONPVARSDSVILNLYGPDAP 240
Db 181 NNQSLPVSPRLQLSNGNRTLTLFNTTRNDTASYKETONPVARSDSVILNLYGPDAP 240
Qy 241 TISPLNTSYRSGENLNSCHAAASNPAPQYSWFVNGTFOOSTOELFIPNTVNNSSSYTCQ 300
Db 241 TISPLNTSYRSGENLNSCHAAASNPAPQYSWFVNGTFOOSTOELFIPNTVNNSSSYTCQ 300
Qy 301 AHNSDTGLNRTTNTTITVYAEPPKPFITSNNSNPVEDDAVALTCEPEIQNTTYLWVNN 360
Db 301 AHNSDTGLNRTTNTTITVYAEPPKPFITSNNSNPVEDDAVALTCEPEIQNTTYLWVNN 360
Qy 361 QSLPVSPRLQLSNDNRRTLTLSTVRNDVGPYECGIONELSDHSDPVILNLYGPDPTI 420
Db 361 QSLPVSPRLQLSNDNRRTLTLSTVRNDVGPYECGIONELSDHSDPVILNLYGPDPTI 420
Qy 421 SPSYTYRPGVNLISCHAAASNPAPQYSWMLIDGNIQOHTOELFISNTEKNSGLYTCQAN 480
Db 421 SPSYTYRPGVNLISCHAAASNPAPQYSWMLIDGNIQOHTOELFISNTEKNSGLYTCQAN 480
Qy 481 NSASGHSRTTYKTIIVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWVNGQS 540
Db 481 NSASGHSRTTYKTIIVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLWVNGQS 540

OY 541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTEIISP 600
DB 541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTEIISP 600
OY 601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQOHTQVLFIAKTTNNNGTYACFVSNL 660
DB 601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQOHTQVLFIAKTTNNNGTYACFVSNL 660
OY 661 ATGRNNSIVKSTIVSASGTPGLSAGATVGMIGVLVVALI 702
DB 661 ATGRNNSIVKSTIVSASGTPGLSAGATVGMIGVLVVALI 702
RESULT 4
ADA84059
ID ADA84059 standard; protein; 702 AA.
AC ADA84059;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human CEA/CAM5 protein.
XX
KW human; marker; expressed sequence tag; EST; arabidopsis; tumour;
KW stress-induced phenotype; hyperosmotic stress; colon cancer; immunogen;
KW vaccine.
XX
OS Homo sapiens.
XX
PN WO2002103028-A2.
XX
PD 27-DEC-2002.
XX
PF 30-MAY-2002; 2002WO-IB004189.
XX
PR 30-MAY-2001; 2001US-0293999P.
XX
PR 22-OCT-2001; 2001US-0330457P.
XX
PR 19-FEB-2002; 2002US-0357144P.
XX
PA (BIOM-) BIOMEDICAL CENT.
XX
PI Baranova AV, Yankovsky NK, Kozlov AP, Lobashev AV, Krukovskaya LL;
XX
DR MPI; 2003-175241/17.
XX
DR N-PSDB; ADA84058.
XX
PT Determining if a nucleic acid is a marker for a phenotype/cell type of
PT interest, by global comparison of expressed sequence tags known to be
PT expressed in the phenotype/cell type with all ESTs expressed in normal
PT tissue.
XX
PS Claim 29; Page 437-440; 516pp; English.
XX
XX The invention relates to a novel method for determining if a nucleic acid
CC is a marker for a predetermined phenotype/cell type of interest from a
CC biological species. The method comprises performing a global comparison
CC of a group of expressed sequence tags (ESTs) known to be expressed in the
CC phenotype/cell type of interest with all ESTs expressed in normal tissue
CC in order to identify ESTs that are preferentially expressed in the
CC phenotype/cell of interest. A method of the invention is useful for
CC determining whether a nucleic acid is a marker for a predetermined
CC phenotype or cell type of interest from a biological species, preferably
CC Arabidopsis or human. The cell type of interest is an abnormal cell such
CC as a tumour cell, and the predetermined phenotype is a stress-induced
CC phenotype such as hyperosmotic stress or high salt conditions. A method
CC of the invention is also useful for determining the progression of colon
CC cancer in a human, for detecting a tumour cell, and for regulating or
CC preventing the growth of a tumour cell. An antibody of the invention is
CC useful for detecting the absence or presence of peptides encoded by
CC tumour-associated markers. A polypeptide of the invention is useful as an
CC immunogen for vaccinating an animal. The present sequence represents a
CC tumour-associated antigen of the invention.

XX
SQ Sequence 702 AA;
Query Match 100.0%; Score 3721; DB 6; Length 702;
Best Local Similarity 100.0%; Pred. No. 1,4e-199;
Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MESPAPPHRWCIPQORLLTLTASLTFPNNPPTAKLTETSTPFNVAEGEVLVHNLQ 60
DB 1 MESPAPPHRWCIPQORLLTLTASLTFPNNPPTAKLTETSTPFNVAEGEVLVHNLQ 60
OY 61 HLFQYSWKGERVDGNROIIIGVICTQOATPGPAYSGEIIYPNASLLIQNTQDGTGY 120
DB 61 HLFQYSWKGERVDGNROIIIGVICTQOATPGPAYSGEIIYPNASLLIQNTQDGTGY 120
OY 121 TLHVIKSDLVNEEAQGFRRVYPELPKPSISSNNSKVEDKDAVAFCEPEODATYLMWV 180
DB 121 TLHVIKSDLVNEEAQGFRRVYPELPKPSISSNNSKVEDKDAVAFCEPEODATYLMWV 180
OY 181 NNQSLPVSPPRLQLSNGNRTLTLFNVTRNDTASVYKCETONPVARSDSVILNLVYGPDPAP 240
DB 181 NNQSLPVSPPRLQLSNGNRTLTLFNVTRNDTASVYKCETONPVARSDSVILNLVYGPDPAP 240
OY 241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQOSTOELTIPNITVNNSGSYTCQ 300
DB 241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQOSTOELTIPNITVNNSGSYTCQ 300
OY 301 AHNSDGILNRTVTITTYAEPKPFITSNNSNPVEDDAVALTCPEPIQNTTYLMMVNN 360
DB 301 AHNSDGILNRTVTITTYAEPKPFITSNNSNPVEDDAVALTCPEPIQNTTYLMMVNN 360
OY 361 QSLPVSPPRLQLSNDNRITLLSVTRNDVGPYECGIQNELSVDSHPVLNLVYGPDDPTI 420
DB 361 QSLPVSPPRLQLSNDNRITLLSVTRNDVGPYECGIQNELSVDSHPVLNLVYGPDDPTI 420
OY 421 SPSTYTYRPGVNLISCHASNPAPQYSWLDGNIQOHTQELFISNITBKNSGLYTCQAN 480
DB 421 SPSTYTYRPGVNLISCHASNPAPQYSWLDGNIQOHTQELFISNITBKNSGLYTCQAN 480
OY 481 NSAGHSRTTYKTIIVSAELPKPSISSNNSKVEDKDAVAFCEPEAONTTYLMMVNGOS 540
DB 481 NSAGHSRTTYKTIIVSAELPKPSISSNNSKVEDKDAVAFCEPEAONTTYLMMVNGOS 540
OY 541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTEIISP 600
DB 541 LPVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVSANRSDPVTLDVLYGPDTEIISP 600
OY 601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQOHTQVLFIAKTTNNNGTYACFVSNL 660
DB 601 PDSSYLSGANLNLSCHSASNPSPQYSWRINGIPQOHTQVLFIAKTTNNNGTYACFVSNL 660
OY 661 ATGRNNSIVKSTIVSASGTPGLSAGATVGMIGVLVVALI 702
DB 661 ATGRNNSIVKSTIVSASGTPGLSAGATVGMIGVLVVALI 702
RESULT 5
ABP74707
ID ABP74707 standard; protein; 702 AA.
AC ABP74707;
XX
DT 03-FEB-2003 (first entry)
XX
DE Human CEA protein SEQ ID NO:592.
XX
XX Human; epitope; vaccine; immunotherapeutic; cytostatic; immunogenicity;
KW T cell.
XX
OS Homo sapiens.
XX
PN WO200281646-A2.
XX

PD 17-OCT-2002.
 XX 04-APR-2002; 2002MO-US011101.
 XX 06-APR-2001; 2001US-0282211P.
 PR 07-NOV-2001; 2001US-0337017P.
 PR 07-MAR-2002; 2002US-0363210P.
 XX (CTL1-) CTL IMMUNOTHERAPIES CORP.
 PA
 XX Simard JTL, Diamond DC, Liu L, Xie Z;
 PI WPI; 2003-067518/06.
 DR N-PSDB; AB083855.
 XX
 XX Novel epitopes useful as vaccines, comprises peptides or nucleic acid
 PT encoding the peptides, that are useful epitopes of target-associated
 PT antigens.
 PS
 PS Claim 1; Page 171; 352pp; English.
 XX
 CC The present invention describes an isolated epitope (I) and an epitope
 CC cluster. Also described is a vaccine or immunotherapeutic composition
 CC (VC) comprising (I). (I) has cytostatic activity. VC is useful for
 CC treating an animal, by administering to an animal the vaccine or
 CC immunotherapeutic composition. VC is also useful for evaluating
 CC immunogenicity of a vaccine or immunotherapeutic composition. By
 CC administering VC to an HLA-transgenic animal and evaluating
 CC immunogenicity based on a characteristic of the animal, or by in vitro
 CC primary stimulation of a T cell and evaluating immunogenicity. (I) is
 CC useful for determining specific T cell frequency, by contacting T cells
 CC with a MHC-peptide complex, and further comprises ELISPOT analysis,
 CC limiting dilution analysis, flow cytometry, in situ hybridisation and/or
 CC polymerase chain reaction (PCR). AB083843 to AB083858 and ABP74128 to
 CC ABP74473 represent sequences used in the exemplification of the present
 CC invention
 CC
 XX
 XX Sequence 702 AA;

Query Match 100.0%; Score 3721; DB 6; Length 702;
 Best Local Similarity 100.0%; Pred. No. 1,4e-199;
 Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSAPHRWCIMWQRLTLTASLLTFWNPPTAKLTIESPPNVAEKEVLLVHNL PQ 60
 DB 1 MESSAPHRWCIMWQRLTLTASLLTFWNPPTAKLTIESPPNVAEKEVLLVHNL PQ 60
 QY HLFYSWYKGRVDGNROIIGVIGTQOATGPAVSGREIITYPNASLLIIONIQNDGFY 120
 DB 61 HLFYSWYKGRVDGNROIIGVIGTQOATGPAVSGREIITYPNASLLIIONIQNDGFY 120
 QY 121 TLHAVIKSDLVNEEATGQFRVYBELPKPSISSNSKPVEDKDAVAFCEPETQDAYLMWV 180
 DB 121 TLHAVIKSDLVNEEATGQFRVYBELPKPSISSNSKPVEDKDAVAFCEPETQDAYLMWV 180
 QY 181 NNQSLPVSPRLQLSNGRRTLLFNVTRNDTASYKCETONPVSARSDSVLIANTYGPDPAP 240
 DB 181 NNQSLPVSPRLQLSNGRRTLLFNVTRNDTASYKCETONPVSARSDSVLIANTYGPDPAP 240
 QY 241 TISPLANTSYRSGENLANSCHAASNPAPQYSWFGVNGTFOQSFOELFIPPIITNNSSGYTCQ 300
 DB 241 TISPLANTSYRSGENLANSCHAASNPAPQYSWFGVNGTFOQSFOELFIPPIITNNSSGYTCQ 300
 QY 301 AHNSDTGLNRTTITTYVAPPKPFTISNNSNPVEDDAVALTCEPEIQNTTYLMMVNN 360
 DB 301 AHNSDTGLNRTTITTYVAPPKPFTISNNSNPVEDDAVALTCEPEIQNTTYLMMVNN 360
 QY 361 QSLPVSPRLQLSNGRRTLLFNVTRNDVGPPECGIQNELSVDSHSDPVYLIANTYGPDPPTI 420
 DB 361 QSLPVSPRLQLSNGRRTLLFNVTRNDVGPPECGIQNELSVDSHSDPVYLIANTYGPDPPTI 420
 QY 421 SPSYTYRPGVNLISLSCHAASNPAPQYSWMLIDGNIQOHTOELFISNTEKNSGLYTCQAN 480
 DB 421 SPSYTYRPGVNLISLSCHAASNPAPQYSWMLIDGNIQOHTOELFISNTEKNSGLYTCQAN 480

DB 421 SPSYTYRPGVNLISLSCHAASNPAPQYSWMLIDGNIQOHTOELFISNTEKNSGLYTCQAN 480
 QY 481 NSASGSHRTYKTTIVSALELPKPSISSNSKPVEDKDAVAFCEPEAQNTTYLMMVNGOS 540
 DB 481 NSASGSHRTYKTTIVSALELPKPSISSNSKPVEDKDAVAFCEPEAQNTTYLMMVNGOS 540
 QY 541 LPVSPRLQLSNGRRTLLFNVTRNDARAYVCGIQNSVSANSDPTLVLVYGPDPPIISP 600
 DB 541 LPVSPRLQLSNGRRTLLFNVTRNDARAYVCGIQNSVSANSDPTLVLVYGPDPPIISP 600
 QY 601 PDSSTLSGANLNSCHASANSPQYSWRINGIPOOHTOVLFIAKITPNNNGTYACFVSUL 660
 DB 601 PDSSTLSGANLNSCHASANSPQYSWRINGIPOOHTOVLFIAKITPNNNGTYACFVSUL 660
 QY 661 ATGRNNSIVKSIITYVASAGTSPGLSAGATVGMIGVLVGVALLI 702
 DB 661 ATGRNNSIVKSIITYVASAGTSPGLSAGATVGMIGVLVGVALLI 702
 RESULT 6
 ABU04837
 ID ABU04837 standard; protein; 702 AA.
 XX
 AC ABU04837;
 XX
 DT 29-JAN-2003 (first entry)
 DE
 DE Human expressed protein tag (EPT) #1503.
 XX
 KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.
 XX
 OS Homo sapiens.
 XX
 XX WO200278524-A2.
 XX
 XX 10-OCT-2002.
 XX
 XX 28-MAR-2002; 2002MO-US009671.
 XX
 XX 28-MAR-2001; 2001US-0279495P.
 PR 21-MAY-2001; 2001US-0292544P.
 PR 08-AUG-2001; 2001US-0310801P.
 PR 01-OCT-2001; 2001US-0326370P.
 PR 04-DEC-2001; 2001US-0336780P.
 PR 20-FEB-2002; 2002US-0358985P.
 XX
 PA (ZYCO-) ZYCOS INC.
 XX
 PI Chicx RM, Tomlinson AJ, Urban RG;
 XX
 XX WPI; 2003-040607/03.
 XX
 XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 XX cytoskeletal proteins, receptors or transcription factors), useful for
 XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 XX leukemia.
 XX
 XX Example 2; SEQ ID NO 1503; 134pp; English.
 XX
 CC The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing

CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX
 XX
 SQ Sequence 702 AA;

Query Match 100.0%; Score 3721; DB 6; Length 702;
 Best Local Similarity 100.0%; Pred. No. 1.4e-199;
 Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESPSAPPHRMCI PMORLLTSLTFNNPPTAKLTISTEPNVAEGEVLVHNLPQ 60
 DB 1 MESPSAPPHRMCI PMORLLTSLTFNNPPTAKLTISTEPNVAEGEVLVHNLPQ 60
 QY 61 HLFQSWYKGERVDGNRQIIIGVIGTQATPGPAVSGREIIPNLSLIIQNIQNDTGFY 120
 DB 61 HLFQSWYKGERVDGNRQIIIGVIGTQATPGPAVSGREIIPNLSLIIQNIQNDTGFY 120
 QY 121 TLHAVIKSDLVNEATGQFRVYPELPKPSISSNNSKVEDKDAVAFTCEBETODATYLMVY 180
 DB 121 TLHAVIKSDLVNEATGQFRVYPELPKPSISSNNSKVEDKDAVAFTCEBETODATYLMVY 180
 QY 181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASVYKCTQNPVSARRSDSYILNVLYGPDAP 240
 DB 181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASVYKCTQNPVSARRSDSYILNVLYGPDAP 240
 QY 241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWPNVGTFOOSTOELFIENITVNNSGSYTQ 300
 DB 241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWPNVGTFOOSTOELFIENITVNNSGSYTQ 300
 QY 301 AHNSDTGLNRTTYTTTVAEPPKPEITSNNSNPVEDDAVALTCBEIQTNTYLMWVN 360
 DB 301 AHNSDTGLNRTTYTTTVAEPPKPEITSNNSNPVEDDAVALTCBEIQTNTYLMWVN 360
 QY 361 QSLPVSPRLQLSNDNRTLTLSTVRNDVGYECGIONELSVBDSVILNVLYGPDPTI 420
 DB 361 QSLPVSPRLQLSNDNRTLTLSTVRNDVGYECGIONELSVBDSVILNVLYGPDPTI 420
 QY 421 SPSTYTPRGVNLISLSCHAASNPPAQYSWLDGNIQOHTOELFISNITEKNSGLYTQAN 480
 DB 421 SPSTYTPRGVNLISLSCHAASNPPAQYSWLDGNIQOHTOELFISNITEKNSGLYTQAN 480
 QY 481 NSASGHSRTTVKTTTYSABELPKPSISSNNSKVEDKDAVAFTCEBETODATYLMWVN 540
 DB 481 NSASGHSRTTVKTTTYSABELPKPSISSNNSKVEDKDAVAFTCEBETODATYLMWVN 540
 QY 541 LPLVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVANSRSDPYTLVLYGPDPIIS 600
 DB 541 LPLVSPRLQLSNGNRTLTLFNVTRNDARAYVCGIQNSVANSRSDPYTLVLYGPDPIIS 600
 QY 601 POSSYLSGANLNLSCHASNPSPQYSWRINGIPQOHTOVLFIKITTNNNGTYACFVSNL 660
 DB 601 POSSYLSGANLNLSCHASNPSPQYSWRINGIPQOHTOVLFIKITTNNNGTYACFVSNL 660
 QY 661 ATGRNNSIVKSTIVSASGTSFGLSAGATVGMIGLVGVALI 702
 DB 661 ATGRNNSIVKSTIVSASGTSFGLSAGATVGMIGLVGVALI 702

RESULT 7

ID ABU04800 standard; protein; 702 AA.

XX ABU04800;

DT 29-JAN-2003 (first entry)

XX Human expressed protein tag (EPT) #1466.

XX

KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

OS Homo sapiens.

XX MO200278524-A2.

XX 10-OCT-2002.

XX 28-MAR-2002; 2002WO-US009671.

XX 28-MAR-2001; 2001US-0279495P.

XX 21-MAY-2001; 2001US-0292544P.

XX 08-AUG-2001; 2001US-0310801P.

XX 01-OCT-2001; 2001US-0326370P.

XX 04-DEC-2001; 2001US-0336780P.

XX 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCO INC.

XX Chicz RM, Tomlinson AJ, Urban RG;

XX WPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.

XX Example 2; SEQ ID NO 1466; 134pp; English.

CC The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX
 XX
 SQ Sequence 702 AA;

Query Match 100.0%; Score 3721; DB 6; Length 702;
 Best Local Similarity 100.0%; Pred. No. 1.4e-199;
 Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESPSAPPHRMCI PMORLLTSLTFNNPPTAKLTISTEPNVAEGEVLVHNLPQ 60
 DB 1 MESPSAPPHRMCI PMORLLTSLTFNNPPTAKLTISTEPNVAEGEVLVHNLPQ 60
 QY 61 HLFQSWYKGERVDGNRQIIIGVIGTQATPGPAVSGREIIPNLSLIIQNIQNDTGFY 120
 DB 61 HLFQSWYKGERVDGNRQIIIGVIGTQATPGPAVSGREIIPNLSLIIQNIQNDTGFY 120
 QY 121 TLHAVIKSDLVNEATGQFRVYPELPKPSISSNNSKVEDKDAVAFTCEBETODATYLMVY 180
 DB 121 TLHAVIKSDLVNEATGQFRVYPELPKPSISSNNSKVEDKDAVAFTCEBETODATYLMVY 180
 QY 181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASVYKCTQNPVSARRSDSYILNVLYGPDAP 240
 DB 181 NNQSLPVSPRLQLSNGNRTLTLFNVTRNDTASVYKCTQNPVSARRSDSYILNVLYGPDAP 240

QY 241 TISPLNTSYRSGENINLSCHASANPPAOYSWFVNGTFOOSTOELFIPNITVNNSSYTCQ 300
DB 241 TISPLNTSYRSGENINLSCHASANPPAOYSWFVNGTFOOSTOELFIPNITVNNSSYTCQ 300
QY 301 AHNSDTGLNRTTITVTVAAEPKPFITSNNSNPVEDDAVALTCEPEIQNTTYLMWVNN 360
DB 301 AHNSDTGLNRTTITVTVAAEPKPFITSNNSNPVEDDAVALTCEPEIQNTTYLMWVNN 360
QY 361 QSLPVSRLQSLNDNRRTLLSVTRNDVGPYECGIONELSVHSDPVIINLVLYGDDPTI 420
DB 361 QSLPVSRLQSLNDNRRTLLSVTRNDVGPYECGIONELSVHSDPVIINLVLYGDDPTI 420
QY 421 SPSYTYRPGVNLISCHASANPPAOYSWLIDGNIQOHTOELFISNITEKNSGLTYCOAN 480
DB 421 SPSYTYRPGVNLISCHASANPPAOYSWLIDGNIQOHTOELFISNITEKNSGLTYCOAN 480
QY 481 NSASGHSRTTYKTTIVSAELPKPSISSNNSKPEVDKDAVAFTCEPEAQNTTYLMWVNGQS 540
DB 481 NSASGHSRTTYKTTIVSAELPKPSISSNNSKPEVDKDAVAFTCEPEAQNTTYLMWVNGQS 540
QY 541 LPVSPRLQSLNGNRTLLFNTVRNDARAYVCGIQNSVSANRSDPYTLDLVLYGDDPTIISP 600
DB 541 LPVSPRLQSLNGNRTLLFNTVRNDARAYVCGIQNSVSANRSDPYTLDLVLYGDDPTIISP 600
QY 601 PDSSYLSGANINLSCHASANPPAOYSWRINGIPOOHTOVLFIKTIPTNNNGTYACFVSNL 660
DB 601 PDSSYLSGANINLSCHASANPPAOYSWRINGIPOOHTOVLFIKTIPTNNNGTYACFVSNL 660
QY 661 ATGRNNSIVKSIITVASAGTSPGLSAGATVGMIGVLVVALI 702
DB 661 ATGRNNSIVKSIITVASAGTSPGLSAGATVGMIGVLVVALI 702

RESULT 8
ABU04834 standard; protein; 702 AA.
ID ABU04834
XX AC ABU04834;
XX DT 29-JAN-2003 (first entry)
XX DE Human expressed protein tag (EPT) #1500.
XX KM Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KM protease; protease inhibitor; transporter; cytoskeletal protein;
KM receptor; transcription factor; cancer; MHC;
KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX OS Homo sapiens.
XX PN MO200278524-A2.
XX PD 10-OCT-2002.
XX PF 28-MAR-2002; 2002WO-US009671.
XX PR 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX PR 01-OCT-2001; 2001US-0326370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002US-0358985P.
XX PA (ZYCO-) ZYCOs INC.
XX PI Chicx RM, Tomlinson AJ, Urban RG;
XX DR WPI; 2003-040607/03.
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for

PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX PS Example 2; SEQ ID NO 1500; 134pp; English.
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for creating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 702 AA;

Query Match 100.0%; Score 3721; DB 6; Length 702;
Best Local Similarity 100.0%; Pred. No. 1,46-199;
Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESPAAPHRCIPQORLLITASLLTFNNPPTAKLTIESPPFNAEGKEVLLVHNLPO 60
DB 1 MESPAAPHRCIPQORLLITASLLTFNNPPTAKLTIESPPFNAEGKEVLLVHNLPO 60
QY 61 HLFYSWKGERVDGNROIGVIGTQOATPEPAYSGREIIPNASLLIQNIIONDTGXY 120
DB 61 HLFYSWKGERVDGNROIGVIGTQOATPEPAYSGREIIPNASLLIQNIIONDTGXY 120
QY 121 TLHVIKSDLVNBEATGQFRVYBELPKPSISSNNSKPEVDKDAVAFTCEPEITDATTYLMWV 180
DB 121 TLHVIKSDLVNBEATGQFRVYBELPKPSISSNNSKPEVDKDAVAFTCEPEITDATTYLMWV 180
QY 181 NNOSLPVSPRLQSLNGNRTLLFNTVRNDTASYKETONPVARSRSVYILNLVLYGDDAP 240
DB 181 NNOSLPVSPRLQSLNGNRTLLFNTVRNDTASYKETONPVARSRSVYILNLVLYGDDAP 240
QY 241 TISPLNTSYRSGENINLSCHASANPPAOYSWFVNGTFOOSTOELFIPNITVNNSSYTCQ 300
DB 241 TISPLNTSYRSGENINLSCHASANPPAOYSWFVNGTFOOSTOELFIPNITVNNSSYTCQ 300
QY 301 AHNSDTGLNRTTITVTVAAEPKPFITSNNSNPVEDDAVALTCEPEIQNTTYLMWVNN 360
DB 301 AHNSDTGLNRTTITVTVAAEPKPFITSNNSNPVEDDAVALTCEPEIQNTTYLMWVNN 360
QY 361 QSLPVSRLQSLNDNRRTLLSVTRNDVGPYECGIONELSVHSDPVIINLVLYGDDPTI 420
DB 361 QSLPVSRLQSLNDNRRTLLSVTRNDVGPYECGIONELSVHSDPVIINLVLYGDDPTI 420
QY 421 SPSYTYRPGVNLISCHASANPPAOYSWLIDGNIQOHTOELFISNITEKNSGLTYCOAN 480
DB 421 SPSYTYRPGVNLISCHASANPPAOYSWLIDGNIQOHTOELFISNITEKNSGLTYCOAN 480
QY 481 NSASGHSRTTYKTTIVSAELPKPSISSNNSKPEVDKDAVAFTCEPEAQNTTYLMWVNGQS 540
DB 481 NSASGHSRTTYKTTIVSAELPKPSISSNNSKPEVDKDAVAFTCEPEAQNTTYLMWVNGQS 540
QY 541 LPVSPRLQSLNGNRTLLFNTVRNDARAYVCGIQNSVSANRSDPYTLDLVLYGDDPTIISP 600
DB 541 LPVSPRLQSLNGNRTLLFNTVRNDARAYVCGIQNSVSANRSDPYTLDLVLYGDDPTIISP 600
QY 601 PDSSYLSGANINLSCHASANPPAOYSWRINGIPOOHTOVLFIKTIPTNNNGTYACFVSNL 660
DB 601 PDSSYLSGANINLSCHASANPPAOYSWRINGIPOOHTOVLFIKTIPTNNNGTYACFVSNL 660

QY 661 ATGRNNSIVKSITVSASGTPGLSAGATVGMIGLVGVALI 702
 |||
 DB 661 ATGRNNSIVKSITVSASGTPGLSAGATVGMIGLVGVALI 702

RESULT 9
 ID AB004796
 AB004796 standard; protein; 702 AA.

AC AB004796;

XX 29-JAN-2003 (first entry)

DE Human expressed protein tag (EPT) #1462.

KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.

XX Homo sapiens.

PN WO200278524-A2.

PD 10-OCT-2002.

PF 28-MAR-2002; 2002WO-US009671.

PR 28-MAR-2001; 2001US-0279495P.

PR 21-MAY-2001; 2001US-0292544P.

PR 08-AUG-2001; 2001US-0310801P.

PR 01-OCT-2001; 2001US-0326370P.

PR 04-DEC-2001; 2001US-0336780P.

PR 20-FEB-2002; 2002US-0358985P.

XX (ZYCO-) ZYCOS INC.

XX Chicz RM, Tomlinson AJ, Urban RG;

XX MPI; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.

XX Example 2; SEQ ID NO 1462; 134pp; English.

XX The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_poc_sequences

XX Sequence 702 AA;

Query Match 100.0%; Score 3721; DB 6; Length 702;
 Best Local Similarity 100.0%; Pred. No. 1.4e-199;
 Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESPAPPHRMCIPIWQRLTLTASLLTFMNPPTTAKLTIESPPNVAEGKEVLLVHNLPO 60
 DB 1 MESPAPPHRMCIPIWQRLTLTASLLTFMNPPTTAKLTIESPPNVAEGKEVLLVHNLPO 60
 QY 61 HLFQYVSWYKGERVDNRQIIGVICTQATPGPAYSGBEIIYPNASSLIQNIIONDTGXY 120
 DB 61 HLFQYVSWYKGERVDNRQIIGVICTQATPGPAYSGBEIIYPNASSLIQNIIONDTGXY 120
 QY 121 TLHVIKSDLVNEATGQFRVYPELPKPSISSNNSKPEVDKDAVAFCEPETODATYLMVY 180
 DB 121 TLHVIKSDLVNEATGQFRVYPELPKPSISSNNSKPEVDKDAVAFCEPETODATYLMVY 180
 QY 181 NNQSLPVSPRLQSLNGNRITLTFNTRNDTASVYKCEQNPVSARRSDVILNLVYGPDPAP 240
 DB 181 NNQSLPVSPRLQSLNGNRITLTFNTRNDTASVYKCEQNPVSARRSDVILNLVYGPDPAP 240
 QY 241 TISPLNTSYRSGENLNLSCHAASNPPAOYSWVNGTFOOSTOELFIPNITVNNSSSYTCQ 300
 DB 241 TISPLNTSYRSGENLNLSCHAASNPPAOYSWVNGTFOOSTOELFIPNITVNNSSSYTCQ 300
 QY 301 AHNSDTGLNRTVTVTITVYAEPPKPFITSNNSNPVEDDVAVALTCEPEIQNTTYLMMVNN 360
 DB 301 AHNSDTGLNRTVTVTITVYAEPPKPFITSNNSNPVEDDVAVALTCEPEIQNTTYLMMVNN 360
 QY 361 QSLPVSPRLQSLNDNRITLTLSTRNVDVGYECGIQNELSVDAHSDPVILNLVYGPDDPTI 420
 DB 361 QSLPVSPRLQSLNDNRITLTLSTRNVDVGYECGIQNELSVDAHSDPVILNLVYGPDDPTI 420
 QY 421 SPSTYTYRPGVNLISCHAAASNPPAOYSWLDIGNIQOHTQELFISNITEKNSGLYTCQAN 480
 DB 421 SPSTYTYRPGVNLISCHAAASNPPAOYSWLDIGNIQOHTQELFISNITEKNSGLYTCQAN 480
 QY 481 NSASGHSRTTYVTITVSAELPKPSISSNNSKPEVDKDAVAFCEPEAQNTTYLMMVNGQS 540
 DB 481 NSASGHSRTTYVTITVSAELPKPSISSNNSKPEVDKDAVAFCEPEAQNTTYLMMVNGQS 540
 QY 541 LPVSPRLQSLNGNRITLTFNTRNDARAIVCGIQNSVSNRSDPYTLDLVYGPDPPIISP 600
 DB 541 LPVSPRLQSLNGNRITLTFNTRNDARAIVCGIQNSVSNRSDPYTLDLVYGPDPPIISP 600
 QY 601 PDSSYLSGANLNLSCHASNPSPQYSWRINGIPQOHTQVLFIAKTTNNNGTYACFVSNTL 660
 DB 601 PDSSYLSGANLNLSCHASNPSPQYSWRINGIPQOHTQVLFIAKTTNNNGTYACFVSNTL 660
 QY 661 ATGRNNSIVKSITVSASGTPGLSAGATVGMIGLVGVALI 702
 DB 661 ATGRNNSIVKSITVSASGTPGLSAGATVGMIGLVGVALI 702

RESULT 10
 ABR82476
 ID ABR82476 standard; protein; 702 AA.
 AC ABR82476;
 XX 20-NOV-2003 (first entry)
 DE Human carcinoembryonic antigen (CEA) polypeptide.
 XX CEA; immune response; carcinoembryonic antigen; antigen presenting cell;
 KW APC; cytostatic; vaccine; human; antigen.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..34
 FT Protein /note= "signal peptide"
 FT /note= "mature protein"
 PN WO2003059379-A2.
 XX 24-JUL-2003.

XX 17-JAN-2003; 2003WO-DK000031.
 XX
 XX 17-JAN-2002; 2002DK-00000082.
 PR 17-JAN-2002; 2002US-0350047P.
 XX
 XX (PHAR-) PHARMEA AS.
 PA
 XX Klyener S, Voldborg B;
 XX
 XX WPI; 2003-587260/55.
 DR
 DR N-PSDB; ACF35963.
 XX
 XX
 PT Inducing an immune response in humans against autologous carcinoembryonic
 PT antigen (CEA) comprises administering a modified CEA polypeptide, a
 PT nucleic acid encoding the polypeptide, or a microorganism expressing the
 PT polypeptide.
 PS
 PS Claim 19; Page 100-104; 140pp; English.
 XX
 CC The invention relates to inducing an immune response against autologous
 CC carcinoembryonic antigen (CEA) in an animal, e.g. human. The method
 CC involves effecting uptake and processing by antigen presenting cells
 CC (APCs) in the animal of at least 1 modified CEA polypeptide or of a
 CC nucleic acid encoding the modified CEA polypeptide or of a microorganism
 CC or virus expressing the modified CEA polypeptide to induce a CTL response
 CC and an antibody response that targets the autologous CEA. The method is
 CC useful in immunizing actively against diseases characterized by cells
 CC that express CEA. The present sequence represents a human CEA polypeptide
 XX
 SQ Sequence 702 AA;

Query Match 100.0%; Score 3721; DB 7; Length 702;
 Best Local Similarity 100.0%; Pred. No. 1,4e-199;
 Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESPSAPPHRCIMFQORLLTASLLTFMNPPTAKLTTESTPENVAGKEVLLVHNLPO 60
 DB 1 MESPSAPPHRCIMFQORLLTASLLTFMNPPTAKLTTESTPENVAGKEVLLVHNLPO 60
 QY 61 HLFYSWYKGERVDGNRQIIIGYVIGTOQATPGPAYSGREIIYPNASSLLIIONIDTGFY 120
 DB 61 HLFYSWYKGERVDGNRQIIIGYVIGTOQATPGPAYSGREIIYPNASSLLIIONIDTGFY 120
 QY 121 TLHAIKDDVNEAKTGQFRVYPELPKPSISSNSKPVEDKDAVAFTCEPETQDATYLMWV 180
 DB 121 TLHAIKDDVNEAKTGQFRVYPELPKPSISSNSKPVEDKDAVAFTCEPETQDATYLMWV 180
 QY 121 TLHAIKDDVNEAKTGQFRVYPELPKPSISSNSKPVEDKDAVAFTCEPETQDATYLMWV 180
 DB 121 TLHAIKDDVNEAKTGQFRVYPELPKPSISSNSKPVEDKDAVAFTCEPETQDATYLMWV 180
 QY 181 NNOSLPVSPRLQLSNGNRTTLFNTVRNDTASYKCEIOTNPVSARSDSVIINLVYGPDPAP 240
 DB 181 NNOSLPVSPRLQLSNGNRTTLFNTVRNDTASYKCEIOTNPVSARSDSVIINLVYGPDPAP 240
 QY 241 TISPLANTSYRSGENILNSCHAASNPQAQYSWFGVNGTFOQSTOELFIPNITVNNSGSYTCQ 300
 DB 241 TISPLANTSYRSGENILNSCHAASNPQAQYSWFGVNGTFOQSTOELFIPNITVNNSGSYTCQ 300
 QY 301 AHNSDTGLNRTTITTYAEPKPFITSSNSNPEVEDADALVTCPEPIQNTTYTLYMWNV 360
 DB 301 AHNSDTGLNRTTITTYAEPKPFITSSNSNPEVEDADALVTCPEPIQNTTYTLYMWNV 360
 QY 361 OSLPVSPRLQLSNGNRTTLTISVTRNDVGPYECGIONELSDHSDPVLINLVYGPDPPTI 420
 DB 361 OSLPVSPRLQLSNGNRTTLTISVTRNDVGPYECGIONELSDHSDPVLINLVYGPDPPTI 420
 QY 421 SPSTYTYRPGVNLISLSCHAASNPQAQYSWMLDGNIOQHTOELFISNTEKSGLYTQCAN 480
 DB 421 SPSTYTYRPGVNLISLSCHAASNPQAQYSWMLDGNIOQHTOELFISNTEKSGLYTQCAN 480
 QY 481 NSASGHSRTTYKTTTVAELPKPSISSNSKPVEDKDAVAFTCEPEAKNTTYTLYMWNV 540
 DB 481 NSASGHSRTTYKTTTVAELPKPSISSNSKPVEDKDAVAFTCEPEAKNTTYTLYMWNV 540
 QY 541 LPVSPRLQLSNGNRTTLFNTVRNDARAYVCGIONSVANSNDPVTILDVLYGPDPPTI 600

DB 541 LPVSPRLQLSNGNRTTLFNTVRNDARAYVCGIONSVANSNDPVTILDVLYGPDPPTI 600
 QY 601 PDSSYLSGANINLSCHASASNPSPQYSWRINGIPOQHTOVLFIKLTTPNNGTYACFVSNL 660
 DB 601 PDSSYLSGANINLSCHASASNPSPQYSWRINGIPOQHTOVLFIKLTTPNNGTYACFVSNL 660
 QY 661 ATGRNNSIVKSIITVSASGTSRGLSAGATVGMIGLVGVALLI 702
 DB 661 ATGRNNSIVKSIITVSASGTSRGLSAGATVGMIGLVGVALLI 702

RESULT 11
 ADC09591
 ID ADC09591 standard; protein; 702 AA.
 XX
 AC ADC09591;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DB CEA protein #SEQ ID 592.
 XX
 KW Epitope; immunological; vaccine;
 KW major histocompatibility complex class I; MHC class I; cancer;
 KW immunisation.
 XX
 OS unidentified.
 XX
 PN WO2003008537-A2.
 XX
 PD 30-JAN-2003.
 XX
 PF 29-MAR-2002; 2002WO-US010189.
 XX
 PR 06-APR-2001; 2001US-0282211P.
 PR 07-NOV-2001; 2001US-0337017P.
 PR 07-MAR-2002; 2002US-0363210P.
 XX
 PA (CTL-I-) CTL IMMUNOTHERAPIES CORP.
 XX
 PI Simard JTL, Diamond DC, Liu L, Xie Z;
 XX
 DR WPI; 2003-248010/24.
 XX
 XX
 PT Epitope having high affinity for major histocompatibility complex class I
 PT useful for treating an animal, evaluating immunogenicity of a vaccine or
 PT therapeutic composition and for diagnosing a disease.
 XX
 PS Claim 1; SEQ ID NO 592; 239pp; English.
 XX
 CC The invention relates to an isolated epitope polypeptide that has high
 CC affinity for major histocompatibility complex (MHC) class I, and an
 CC epitope cluster comprising the polypeptide. Also disclosed is a vaccine
 CC or immunotherapeutic composition containing an epitope of the invention.
 CC Compositions of the invention may be used in the treatment of cancer. The
 CC method can be combined with a radiation therapy, chemotherapy,
 CC biochemotherapy or surgery. The composition is also useful for
 CC immunogenicity of a vaccine or immunotherapeutic compound. Multimeric MHC
 CC -peptide complexes of the invention are useful for determining specific T
 CC cell frequency. This method is useful for evaluating immunological
 CC response, by performing the method prior to and subsequent to an
 CC immunisation step. Compositions of the invention are useful for
 CC diagnosing a disease. The current sequence represents an epitope of the
 CC invention with high affinity for MHC class I.
 XX
 SQ Sequence 702 AA;

Query Match 100.0%; Score 3721; DB 7; Length 702;
 Best Local Similarity 100.0%; Pred. No. 1,4e-199;
 Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESPSAPPHRCIMFQORLLTASLLTFMNPPTAKLTTESTPENVAGKEVLLVHNLPO 60
 |||

```

Db      1  MESSPAPPHRWCIPWQRLTLTSLTFFMNPPTAKLTISTPFPNVAEGKEVLLVHNLPQ 60
QY      61  HLFQSWYKGERVDNGROIIGVIGTQOATPGAPVSGREIIPNMSLLQNIIONDTGTY 120
Db      61  HLFQSWYKGERVDNGROIIGVIGTQOATPGAPVSGREIIPNMSLLQNIIONDTGTY 120
QY      121  TLHVKSIDLVDNEATQGFVRYPPELPKPSISSNNSKRVEDKDAVAFTCEPETODATYLMV 180
Db      121  TLHVKSIDLVDNEATQGFVRYPPELPKPSISSNNSKRVEDKDAVAFTCEPETODATYLMV 180
QY      181  NNQSLPVSRLQSLNSGNRTLTFTNTRNDTASYKCTQNPPVARSDSVILNLYGPDAP 240
Db      181  NNQSLPVSRLQSLNSGNRTLTFTNTRNDTASYKCTQNPPVARSDSVILNLYGPDAP 240
QY      241  TISPLTSTRSGENLNLSCHAASNPPAQSWMFVNGFTQOSTDLFPNITVNNSSGYTQ 300
Db      241  TISPLTSTRSGENLNLSCHAASNPPAQSWMFVNGFTQOSTDLFPNITVNNSSGYTQ 300
QY      301  AHNSDTGLNRTTITTYVAEPPKPTISNNSNPVEDDAVALTCEPEIQNTTYLMWVN 360
Db      301  AHNSDTGLNRTTITTYVAEPPKPTISNNSNPVEDDAVALTCEPEIQNTTYLMWVN 360
QY      361  QSLPVSRLQSLNSGNRTLTLLSTNRNDVGPYECGIONELSDHSVPYILNLYGPDPTI 420
Db      361  QSLPVSRLQSLNSGNRTLTLLSTNRNDVGPYECGIONELSDHSVPYILNLYGPDPTI 420
QY      421  SPSTYTRPGVNLSSCHAASNPPAQSWMIDNIGQHTQELFISITEKNSGLYTCQAN 480
Db      421  SPSTYTRPGVNLSSCHAASNPPAQSWMIDNIGQHTQELFISITEKNSGLYTCQAN 480
QY      481  NSAGHSRTTIVKTIIVSAELPKPSISSNNSKRVEDDAVAFTCEPEIQNTTYLMWVN 540
Db      481  NSAGHSRTTIVKTIIVSAELPKPSISSNNSKRVEDDAVAFTCEPEIQNTTYLMWVN 540
QY      541  LVPSPRLQSLNSGNRTLTFTNTRNDARAYVCGIQNSVANRSDPTLDVLYGPDPTI 600
Db      541  LVPSPRLQSLNSGNRTLTFTNTRNDARAYVCGIQNSVANRSDPTLDVLYGPDPTI 600
QY      601  PSSVYSGANLNLSCHAASNPPAQSWMIRNGIPEQHTQVLFIAKTIENNNGTYACVSNL 660
Db      601  PSSVYSGANLNLSCHAASNPPAQSWMIRNGIPEQHTQVLFIAKTIENNNGTYACVSNL 660
QY      661  ATGRNNSIVKSIIVSASGTSPLSAGATVIGIMGVAVLI 702
Db      661  ATGRNNSIVKSIIVSASGTSPLSAGATVIGIMGVAVLI 702

```

```

XX      17-JAN-2001; 2001US-0367358P.
PR      17-JAN-2002; 2002US--00053530.
PR      03-JUN-2002; 2002US-0385691P.
XX      (GENE-) GENE-CRAFT INC.
PA      Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
DR      WPI; 2003-801317/75.
XX      New binding domain-immunoglobulin fusion protein, useful for treating a
PT      subject having or suspected of having a malignant condition or a B-cell
XX      disorder, e.g. melanoma, Grave's disease or autoimmune disease.
XX      Disclosure; SEQ ID NO 87; 157pp; English.
XX      The invention relates to a binding domain-immunoglobulin fusion protein
CC      comprising a binding domain polypeptide that is fused to an
CC      immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain
CC      CH2 constant region polypeptide that is fused to the hinge region
CC      polypeptide, and an immunoglobulin heavy chain CH3 constant region
CC      polypeptide that is fused to the CH2 constant region polypeptide. The
CC      hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin
CC      hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge
CC      region polypeptide, derived from (a) having 3 or more cysteine residues;
CC      where the mutated human IgG1 immunoglobulin hinge region polypeptide
CC      contains 2 cysteine residues, where the first cysteine is not mutated; a
CC      mutated human IgG1 immunoglobulin hinge region polypeptide, derived from
CC      (a) having 3 or more cysteine residues, where the mutated human IgG1
CC      immunoglobulin hinge region polypeptide contains no more than one
CC      cysteine residue; and a mutated human IgG1 immunoglobulin hinge region
CC      polypeptide, derived from (a) having 3 or more cysteine residues; where
CC      the mutated human IgG1 immunoglobulin hinge region polypeptide contains
CC      no cysteine residues. The binding domain-immunoglobulin fusion protein is
CC      capable of at least one immunological activity comprising antibody
CC      dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The
CC      binding domain polypeptide is capable of specifically binding to an
CC      antigen. Also included are an isolated polynucleotide encoding the
CC      binding domain-immunoglobulin fusion protein, a recombinant expression
CC      construct comprising the polynucleotide (operably linked to a promoter),
CC      a host cell transformed or transfected with a recombinant expression
CC      construct, producing the binding domain-immunoglobulin fusion protein, a
CC      pharmaceutical composition comprising the binding domain-immunoglobulin
CC      fusion protein or polynucleotide and a carrier, and treating a subject
CC      having or suspected of having a malignant condition or a B-cell disorder.
CC      The binding domain-immunoglobulin fusion protein is useful for treating a
CC      subject having or suspected of having a malignant condition or a B-cell
CC      disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,
CC      myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple
CC      sclerosis or autoimmune disease. The present sequence is a binding domain
CC      -immunoglobulin fusion protein-associated protein sequence. Note: The
CC      sequence data for this patent formed part of the printed specification
CC      and is also available in electronic format directly from USPTO at
CC      seqdata.uspto.gov/sequence.html?DocId=20030118592. The authors have not
CC      identified the sequences in the printed specification by their SEQ ID
CC      number therefore none of the sequences can be explicitly identified.
XX      Sequence 702 AA;
SQ

```

```

Query Match      100.0%; Score 3721; DB 7; Length 702;
Best local Similarity 100.0%; Pred. No. 1.4e-199;
Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1  MESSPAPPHRWCIPWQRLTLTSLTFFMNPPTAKLTISTPFPNVAEGKEVLLVHNLPQ 60
Db      1  MESSPAPPHRWCIPWQRLTLTSLTFFMNPPTAKLTISTPFPNVAEGKEVLLVHNLPQ 60
QY      61  HLFQSWYKGERVDNGROIIGVIGTQOATPGAPVSGREIIPNMSLLQNIIONDTGTY 120
Db      61  HLFQSWYKGERVDNGROIIGVIGTQOATPGAPVSGREIIPNMSLLQNIIONDTGTY 120
QY      121  TLHVKSIDLVDNEATQGFVRYPPELPKPSISSNNSKRVEDKDAVAFTCEPETODATYLMV 180

```

```

Db      121 TLHVKSDLVNBEATGQFRVYBELPKPSSNNKSPVEDKQAVAFCEPEQDQATYLMWV 180
Qy      181 NNQSLPVSPPRLQSLNGNRTLTLPNTRNDTASYKCETONPVSARSDSVILNVLGPDAP 240
Db      181 NNQSLPVSPPRLQSLNGNRTLTLPNTRNDTASYKCETONPVSARSDSVILNVLGPDAP 240
Qy      241 TISPLNTSYRSGENLNSCHAASNPAPQYSFVNGTFOOSTOELFIPNITVNNSSGYCQ 300
Db      241 TISPLNTSYRSGENLNSCHAASNPAPQYSFVNGTFOOSTOELFIPNITVNNSSGYCQ 300
Qy      301 AHNSDTGANRTTITTYAABPKPFTSNNSNPVEDDAVALTCEPEIQNTTYLMWVN 360
Db      301 AHNSDTGANRTTITTYAABPKPFTSNNSNPVEDDAVALTCEPEIQNTTYLMWVN 360
Qy      361 QSLPVSPPRLQSLNDNRRTLTLSVTRNDVGPYECGIONELSDHSDPVLNVLGPDPTI 420
Db      361 QSLPVSPPRLQSLNDNRRTLTLSVTRNDVGPYECGIONELSDHSDPVLNVLGPDPTI 420
Qy      421 SPSYTYRPGVNLSLCHAASNPAPQYSWMLDGNIOHTOELFISNTEKNSGLYTCQAN 480
Db      421 SPSYTYRPGVNLSLCHAASNPAPQYSWMLDGNIOHTOELFISNTEKNSGLYTCQAN 480
Qy      481 NSAGSHRTTYKTTVSAELPKPSSNNKSPVEDKQAVAFCEPEAQNTTYLMWVNGQS 540
Db      481 NSAGSHRTTYKTTVSAELPKPSSNNKSPVEDKQAVAFCEPEAQNTTYLMWVNGQS 540
Qy      541 LPVSPRLQSLNGNRTLTLPNTRNDARAYVCGIQNSVSNNSDPYTLNVLGPDPTIISP 600
Db      541 LPVSPRLQSLNGNRTLTLPNTRNDARAYVCGIQNSVSNNSDPYTLNVLGPDPTIISP 600
Qy      601 PDSGYLSGANLNSCHASNPSPQYSWRINGIPOHTOVLFLAKTTPNNGYACFVSNL 660
Db      601 PDSGYLSGANLNSCHASNPSPQYSWRINGIPOHTOVLFLAKTTPNNGYACFVSNL 660
Qy      661 ATGRNNSIVKSIIVASAGTSPGLSAGATVGIMIGLVAVAI 702
Db      661 ATGRNNSIVKSIIVASAGTSPGLSAGATVGIMIGLVAVAI 702

```

RESULT 13
ADD46175
ID ADD46175 standard; protein; 702 AA.

```

AC      ADD46175;
DT      29-JAN-2004 (first entry)
DE      Human Protein P06731, SEQ ID NO 11850.
KW      Human; pain; neuronal tissue; gene therapy;
KW      spinal segmental nerve injury; chronic constriction injury; CCI;
KW      spared nerve injury; SNI; Chung.
OS      Homo sapiens.
PN      NC02003016475-A2.
PD      27-FEB-2003.
PF      14-AUG-2002; 2002MO-US025765.
PR      14-AUG-2001; 2001US-0312147P.
PR      01-NOV-2001; 2001US-0346382P.
PR      26-NOV-2001; 2001US-0333347P.
XX      (GEO ) GEN HOSPITAL CORP.
PA      (FARB ) BAYER AG.
PI      Woolf C, D'Urso D, Befort K, Costigan M;
XX      WPI; 2003-268312/26.
DR      GENBANK; P06731.

```

```

XX      New composition comprising two or more isolated polypeptides, useful for
PT      preparing a medicament for treating pain in an animal.
PS      Claim 1; Page; 1017pp; English.
XX      The invention discloses a composition comprising two or more isolated rat
or human polynucleotides or a polynucleotide which represents a fragment,
derivative or allelic variation of the nucleic acid sequence. Also
claimed are a vector comprising the novel polynucleotide, a host cell
comprising the vector, a method for identifying a nucleotide sequence
which is differentially regulated in an animal subjected to pain and a
kit to perform the method, an array, a method for identifying an agent
that increases or decreases the expression of the polynucleotide sequence
that is differentially expressed in neuronal tissue of a first animal
subjected to pain, a method for identifying a compound which regulates
the expression of a polynucleotide sequence which is differentially
expressed in an animal subjected to pain, a method for identifying a
compound that regulates the activity of one or more of the
polynucleotides, a method for producing a pharmaceutical composition, a
method for identifying a compound or small molecule that regulates the
activity in an animal of one or more of the polypeptides given in the
specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
polypeptides or their antibodies. The polynucleotide or the compound that
modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
therapy). The sequence presented is a human protein (shown in Table 2 of
the specification) which is differentially expressed during pain. Note:
The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic form directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences.

```

Sequence 702 AA:

Query Match 100.0%; Score 3721; DB 7; Length 702;
Best Local Similarity 100.0%; Pred. No. 1.4e-199;
Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 MESPSAPPHRCIMQORLLTASLTTFWNPPTAKLTIESTPFNVAEKEVLLVHNLPQ 60
Db      1 MESPSAPPHRCIMQORLLTASLTTFWNPPTAKLTIESTPFNVAEKEVLLVHNLPQ 60
Qy      61 HLFQSWYKGERVDNROIIIGVIGTQATGPAVSGREIITYPNASLLIQNIQNDTGRY 120
Db      61 HLFQSWYKGERVDNROIIIGVIGTQATGPAVSGREIITYPNASLLIQNIQNDTGRY 120
Qy      121 TLHVKSDLVNBEATGQFRVYBELPKPSSNNKSPVEDKQAVAFCEPEQDQATYLMWV 180
Db      121 TLHVKSDLVNBEATGQFRVYBELPKPSSNNKSPVEDKQAVAFCEPEQDQATYLMWV 180
Qy      181 NNQSLPVSPPRLQSLNGNRTLTLPNTRNDTASYKCETONPVSARSDSVILNVLGPDAP 240
Db      181 NNQSLPVSPPRLQSLNGNRTLTLPNTRNDTASYKCETONPVSARSDSVILNVLGPDAP 240
Qy      241 TISPLNTSYRSGENLNSCHAASNPAPQYSFVNGTFOOSTOELFIPNITVNNSSGYCQ 300
Db      241 TISPLNTSYRSGENLNSCHAASNPAPQYSFVNGTFOOSTOELFIPNITVNNSSGYCQ 300
Qy      301 AHNSDTGANRTTITTYAABPKPFTSNNSNPVEDDAVALTCEPEIQNTTYLMWVN 360
Db      301 AHNSDTGANRTTITTYAABPKPFTSNNSNPVEDDAVALTCEPEIQNTTYLMWVN 360
Qy      361 QSLPVSPPRLQSLNDNRRTLTLSVTRNDVGPYECGIONELSDHSDPVLNVLGPDPTI 420
Db      361 QSLPVSPPRLQSLNDNRRTLTLSVTRNDVGPYECGIONELSDHSDPVLNVLGPDPTI 420
Qy      421 SPSYTYRPGVNLSLCHAASNPAPQYSWMLDGNIOHTOELFISNTEKNSGLYTCQAN 480
Db      421 SPSYTYRPGVNLSLCHAASNPAPQYSWMLDGNIOHTOELFISNTEKNSGLYTCQAN 480
Qy      481 NSAGSHRTTYKTTVSAELPKPSSNNKSPVEDKQAVAFCEPEAQNTTYLMWVNGQS 540

```

DB 481 NSASGHSRTTIVKTTIVSAELPKPSISSNNKPEVEDDAVAFTCEPEAQNTTYLMMVNGQS 540
QY 541 LPSVSPRLQLSNGNRITLTLPNTVRNDARAAYVCGIQNSVSAANRSDPTLVDLYGPDPTIISP 600
DB 541 LPSVSPRLQLSNGNRITLTLPNTVRNDARAAYVCGIQNSVSAANRSDPTLVDLYGPDPTIISP 600
QY 601 PSSSYSGANLNLSCHASNPSPQYSWRINGIPQOHTQVLFIAKITPNNNGTYACFVSNL 660
DB 601 PSSSYSGANLNLSCHASNPSPQYSWRINGIPQOHTQVLFIAKITPNNNGTYACFVSNL 660
QY 661 ATGRNNSIVKSITVSASGTPGLSAGATVGMIGLVGVALI 702
DB 661 ATGRNNSIVKSITVSASGTPGLSAGATVGMIGLVGVALI 702
RESULT 14
ADD84721
ID ADD84721 standard; protein; 702 AA.
AC ADD84721;
XX 29-JAN-2004 (first entry)
DT Human carcinoembryonic antigen (CEA) primary amino acid sequence.
DE
XX
KM identification;
KW class I major histocompatibility complex-binding fragment;
KW class I MHC molecule; class I MHC-binding fragment; cytostatic; cancer;
KW human; carcinoembryonic antigen; CEA; epitope.
OS Synthetic.
OS Homo sapiens.
PN WO2003082317-A1.
XX 09-OCT-2003.
PD 20-MAR-2003; 2003WO-US008427.
PF 22-MAR-2002; 2002US-0366822P.
PR (ZYCO-) ZYCOS INC.
PA (AVET) AVENTIS PASTEUR INC.
XX Chica RM, Tomlinson AJ;
PI WPI; 2003-902907/82.
DR Identifying a class I major histocompatibility complex (MHC)-binding
PT fragment of a polypeptide comprises isolating an MHC molecule, eluting
PT the peptide from the molecule, and identifying the peptide as a
PT polypeptide fragment.
XX Disclosure; Fig 8; 98pp; English.
PS The present invention describes a method for identifying a class I major
XX histocompatibility complex (MHC)-binding fragment of a polypeptide by
CC isolating from the tissue/cell line a class I MHC molecule bound to a
CC peptide, where the peptide is a class I MHC-binding fragment of the
CC polypeptide, eluting the peptide from the class I MHC molecule, and
CC identifying the peptide as a fragment of the polypeptide. A class I MHC-
CC binding fragment has cytostatic activity. Compositions and methods from
CC the present invention can be used in diagnosing, preventing or treating
CC cancer. The method may also be used in identifying peptides involved in
CC the pathogenesis of or protection from diseases associated with
CC expression of class I MHC molecules. The present sequence represents the
CC human carcinoembryonic antigen (CEA) primary amino acid sequence, which
CC is used in the exemplification of the present invention.
XX
XX Sequence 702 AA;
XX
Query Match 100.0%; Score 3721; DB 7; Length 702;

Best Local Similarity 100.0%; Pred. No. 1.4e-199;
Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MESPAPAPPRMRCIPMQRLLTLTSLTFPMNPPTAKLTITESTFPNVAEGEYVLLVHNLPQ 60
DB 1 MESPAPAPPRMRCIPMQRLLTLTSLTFPMNPPTAKLTITESTFPNVAEGEYVLLVHNLPQ 60
QY 61 HIFGYSWYGEAVDNGRQIIGYVIGTQOATPPGASGREIIPNALSLLQNIIONDTGFI 120
DB 61 HIFGYSWYGEAVDNGRQIIGYVIGTQOATPPGASGREIIPNALSLLQNIIONDTGFI 120
QY 121 TLHAVIKSDLVNEATQGFVRYPELKPSPSISNNKSPVEDKDAVAFTCEBETODATYLMV 180
DB 121 TLHAVIKSDLVNEATQGFVRYPELKPSPSISNNKSPVEDKDAVAFTCEBETODATYLMV 180
QY 181 NNQSLPVSFRLQLSNGNRITLTLPNTVRNDTASYKETQNPVARSDSYTLVAVLYGPDAP 240
DB 181 NNQSLPVSFRLQLSNGNRITLTLPNTVRNDTASYKETQNPVARSDSYTLVAVLYGPDAP 240
QY 241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQOSTOELFIPNITVNNSGSYTQ 300
DB 241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWFVNGTFQOSTOELFIPNITVNNSGSYTQ 300
QY 301 AHNSDTGLNRITVTITVYAEPKPFITSNNSNPVEDDAVALTCEPEIQNTTYLMMVNN 360
DB 301 AHNSDTGLNRITVTITVYAEPKPFITSNNSNPVEDDAVALTCEPEIQNTTYLMMVNN 360
QY 361 QSLPVSFRLQLSNDNRITLTLSVTRNDVCPYECGIQNELSVHSDPVLINLYGPDPTI 420
DB 361 QSLPVSFRLQLSNDNRITLTLSVTRNDVCPYECGIQNELSVHSDPVLINLYGPDPTI 420
QY 421 SPSYTYRPGVNLISCHASNPPAQYSWLDIGNIQHTQELFISNTEKNSGLYTQAN 480
DB 421 SPSYTYRPGVNLISCHASNPPAQYSWLDIGNIQHTQELFISNTEKNSGLYTQAN 480
QY 481 NSASGHSRTTIVKTTIVSAELPKPSISSNNKPEVEDDAVAFTCEPEAQNTTYLMMVNGQS 540
DB 481 NSASGHSRTTIVKTTIVSAELPKPSISSNNKPEVEDDAVAFTCEPEAQNTTYLMMVNGQS 540
QY 541 LPSVSPRLQLSNGNRITLTLPNTVRNDARAAYVCGIQNSVSAANRSDPTLVDLYGPDPTIISP 600
DB 541 LPSVSPRLQLSNGNRITLTLPNTVRNDARAAYVCGIQNSVSAANRSDPTLVDLYGPDPTIISP 600
QY 601 PSSSYSGANLNLSCHASNPSPQYSWRINGIPQOHTQVLFIAKITPNNNGTYACFVSNL 660
DB 601 PSSSYSGANLNLSCHASNPSPQYSWRINGIPQOHTQVLFIAKITPNNNGTYACFVSNL 660
QY 661 ATGRNNSIVKSITVSASGTPGLSAGATVGMIGLVGVALI 702
DB 661 ATGRNNSIVKSITVSASGTPGLSAGATVGMIGLVGVALI 702
RESULT 15
ADN39014
ID ADN39014 standard; protein; 702 AA.
XX
XX ADN39014;
AC 17-JUN-2004 (first entry)
DT
XX
DB Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:332.
XX Human; differential expression; cancer; angiogenic disorder;
KW fibrotic disorder; periorbitis; ischemia; heart disease; atherosclerosis;
KW inflammatory disease; autoimmune disease;
KW retinal neovascularization syndrome; scarring; uterine fibroid;
KW detection; diagnosis; prognosis; drug screening; drug targeting;
KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW vulnary; gene therapy; vaccine.
XX
XX Homo sapiens.
XX
XX WO2003042661-A2.


```

XX 22-MAY-2003.
PD 13-NOV-2002; 2002MO-US036810.
XX
PR 13-NOV-2001; 2001US-0350666P.
PR 21-NOV-2001; 2001US-0332464P.
PR 29-NOV-2001; 2001US-0334393P.
PR 03-DEC-2001; 2001US-0335394P.
PR 14-DEC-2001; 2001US-0340376P.
PR 08-JAN-2002; 2002US-0347211P.
PR 10-JAN-2002; 2002US-0347349P.
PR 08-FEB-2002; 2002US-0355250P.
PR 13-FEB-2002; 2002US-0356714P.
PR 20-FEB-2002; 2002US-0359077P.
PR 29-MAR-2002; 2002US-0368809P.
PR 04-APR-2002; 2002US-0370110P.
PR 12-APR-2002; 2002US-0372246P.
PR 05-JUN-2002; 2002US-0386614P.
PR 16-JUL-2002; 2002US-0396839P.
PR 22-JUL-2002; 2002US-0397775P.
PR 22-JUL-2002; 2002US-0397845P.
PR 09-SEP-2002; 2002US-0409450P.
XX
PA (BOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Afar D, Aziz N, Ginsburg WM, Gish KC, Glyme R, Hevezi PA;
PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
XX
DR WPI; 2003-468649/44.
DR N-PSDB; ADN39013.
XX
PT Determining the presence or absence of a pathological cell in a patient,
PT useful for diagnosing, prognosing or treating cancer, comprises detecting
PT a nucleic acid in a biological sample.
XX
PS Claim 12; SEQ ID NO 332; 1385pp; English.
XX
CC The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC whose expression is upregulated or downregulated in specific cancers or
CC other diseases such as angiogenic or fibrotic disorders, and to methods
CC of determining the presence or absence of a pathological cell in a
CC patient by detecting a nucleic acid at least 80% identical to those of
CC the invention or by detecting a polypeptide of the invention. The
CC invention also relates to expression vectors and host cells comprising a
CC nucleic acid of the invention; antibodies which specifically bind a
CC polypeptide of the invention; use of such antibodies for drug targeting;
CC and methods of screening for modulators of activity or expression of the
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC antibodies and methods are useful for diagnosing, prognosing and treating
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC neovascularization syndromes, scarring and uterine fibroids. They may
CC also be useful in wound healing and in contraception. The present
CC sequence represents a polypeptide of the invention.
XX
SQ Sequence 702 AA:

```

```

Query Match 100.0%; Score 3721; DB 7; Length 702;
Best Local Similarity 100.0%; Pred. No. 1,4e-199;
Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MESSAPPHRCIMWOLLLTASLLTFWNPPTAKLTITESTPPRVASGKEYLLVHNLPQ 60
DB 1 MESSAPPHRCIMWOLLLTASLLTFWNPPTAKLTITESTPPRVASGKEYLLVHNLPQ 60
QY 61 HLFQSYWYKGERVDGNROIIIGYVIGTOOATPGPAYSGREIIYPNASLLIONIIIONDTGFY 120
DB 61 HLFQSYWYKGERVDGNROIIIGYVIGTOOATPGPAYSGREIIYPNASLLIONIIIONDTGFY 120
QY 121 TLHVIKSDLVNEATGQFRVYVPELPKPSISSNNSKPYEDKDAVAFTCBPETODATYLMV 180
DB 121 TLHVIKSDLVNEATGQFRVYVPELPKPSISSNNSKPYEDKDAVAFTCBPETODATYLMV 180

```

```

QY 181 NNOGLPVSPRLQLSNGNRTLLFNTRNDTASYKCEONPVASRRSDVILNVLYGPDAP 240
DB 181 NNOGLPVSPRLQLSNGNRTLLFNTRNDTASYKCEONPVASRRSDVILNVLYGPDAP 240
QY 241 TISPLNTSYRGENMLNSCHASNPPOAYSFVNGTFOOSQOELFIPNITVNNSSGYCQ 300
DB 241 TISPLNTSYRGENMLNSCHASNPPOAYSFVNGTFOOSQOELFIPNITVNNSSGYCQ 300
QY 301 AHNSDTGLNRTTITVYAAPPKPFITSNNSNPVEDDAVALTCBPETIONTTYLMVYNN 360
DB 301 AHNSDTGLNRTTITVYAAPPKPFITSNNSNPVEDDAVALTCBPETIONTTYLMVYNN 360
QY 361 QSLPVSPRLQLSNDRITLLSVTRNDVGPYECGIONELSYDHSDPVILNVLYGPDPTI 420
DB 361 QSLPVSPRLQLSNDRITLLSVTRNDVGPYECGIONELSYDHSDPVILNVLYGPDPTI 420
QY 421 SPSTYTYRPGVNLISCHASNPPOAYSMILDGNIOOHTOELFISNTEKNSGLYTCQAN 480
DB 421 SPSTYTYRPGVNLISCHASNPPOAYSMILDGNIOOHTOELFISNTEKNSGLYTCQAN 480
QY 481 NSAGHSRTTYKTIIVSAELPKPSISSNNSKPYEDKDAVAFTCBPETIONTTYLMVYNN 540
DB 481 NSAGHSRTTYKTIIVSAELPKPSISSNNSKPYEDKDAVAFTCBPETIONTTYLMVYNN 540
QY 541 LPVSPRLQLSNGNRTLLFNTRNDARAYVCGIONSVASNSDPVTLVLYGPDPTISP 600
DB 541 LPVSPRLQLSNGNRTLLFNTRNDARAYVCGIONSVASNSDPVTLVLYGPDPTISP 600
QY 601 PDSSYLSGANLNSCHASNPSPQYSWRINGIPQOHTOELFIAKITPPNNGTYACFVSNL 660
DB 601 PDSSYLSGANLNSCHASNPSPQYSWRINGIPQOHTOELFIAKITPPNNGTYACFVSNL 660
QY 661 ATGRNNSIVKSIIVSASGTPGLSAGATVIGIMIGLVGVALI 702
DB 661 ATGRNNSIVKSIIVSASGTPGLSAGATVIGIMIGLVGVALI 702

```

Search completed: April 10, 2006, 18:01:25
Job time : 275.797 secs

"THIS PAGE LEFT BLANK"

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 10, 2006, 18:07:51 ; Search time 179,941 Seconds
(without alignments)
1630.072 Million cell updates/sec

Title: US-10-734-564-72

Perfect score: 3721

Sequence: 1 MESPSAPPHRCIPWQRLLL.....LSAGATGICMIGLVGVALI 702

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3721	100.0	702	US-10-157-031-341	Sequence 341, App
2	3721	100.0	702	US-10-207-655-87	Sequence 87, Appl
3	3721	100.0	702	US-10-117-937-592	Sequence 592, App
4	3721	100.0	702	US-10-295-027-332	Sequence 332, App
5	3721	100.0	702	US-10-245-871-282	Sequence 282, App
6	3721	100.0	702	US-10-253-286-282	Sequence 282, App
7	3721	100.0	702	US-10-380-136-16	Sequence 16, Appl
8	3721	100.0	702	US-10-149-137A-458	Sequence 458, App
9	3721	100.0	702	US-10-712-124-72	Sequence 72, Appl
10	3721	100.0	702	US-10-734-564-72	Sequence 72, Appl
11	3721	100.0	702	US-10-657-022-88	Sequence 88, Appl
12	3721	100.0	702	US-10-473-127-1462	Sequence 1462, App
13	3721	100.0	702	US-10-473-127-1466	Sequence 1466, App
14	3721	100.0	702	US-10-473-127-1500	Sequence 1500, App
15	3721	100.0	702	US-10-473-127-1503	Sequence 1503, App
16	3721	100.0	702	US-10-696-639-65	Sequence 65, Appl
17	3721	100.0	702	US-10-696-639-65	Sequence 65, Appl
18	3721	100.0	702	US-10-482-029-241	Sequence 241, Appl
19	3721	100.0	702	US-10-893-018-2	Sequence 2, Appl
20	3721	100.0	702	US-10-794-514A-301	Sequence 301, Appl
21	3721	100.0	702	US-10-756-149-4748	Sequence 4748, App
22	3721	100.0	702	US-11-067-064-592	Sequence 592, App
23	3721	100.0	702	US-11-067-159-592	Sequence 592, App
24	3721	100.0	702	US-09-756-551A-17	Sequence 17, Appl
25	3721	100.0	702	US-10-473-127-1489	Sequence 1489, App
26	3718	99.9	796	US-10-473-127-1478	Sequence 1478, App
27	3701.5	99.5	701	US-10-168-417A-4	Sequence 4, Appl

28	3700	99.4	698	5	US-10-473-127-1464	Sequence 1464, App
29	3700	99.4	698	5	US-10-473-127-1472	Sequence 1472, App
30	3700	99.4	698	5	US-10-473-127-1488	Sequence 1488, App
31	3700	99.4	698	5	US-10-473-127-1493	Sequence 1493, App
32	3694	99.3	702	5	US-10-473-127-1483	Sequence 1483, App
33	3687	99.1	702	5	US-10-473-127-1485	Sequence 1485, App
34	3687	99.1	702	5	US-10-473-127-1491	Sequence 1491, App
35	3685.5	99.0	697	5	US-10-473-127-1475	Sequence 1475, App
36	3683	99.0	702	5	US-10-473-127-1465	Sequence 1465, App
37	3668	98.6	702	5	US-10-473-127-1496	Sequence 1496, App
38	3643	97.9	698	5	US-10-473-127-1482	Sequence 1482, App
39	3625	97.4	681	5	US-10-893-018-4	Sequence 4, Appl
40	3603	96.8	717	5	US-10-893-018-6	Sequence 6, Appl
41	3565	95.8	713	5	US-10-893-018-10	Sequence 10, Appl
42	3535.5	95.0	708	5	US-10-893-018-8	Sequence 8, Appl
43	3453	92.8	737	3	US-09-925-301-1133	Sequence 1133, Appl
44	3453	92.8	737	5	US-10-473-127-1476	Sequence 1476, App
45	3417	91.8	645	5	US-10-510-523-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-10-157-031-341

Sequence 341, Application US/10157031
Publication No. US20030108890A1

GENERAL INFORMATION:

APPLICANT: Baranova, A. V.

APPLICANT: Yankovsky, N. K.

APPLICANT: Kozlov, A. P.

APPLICANT: Lobashov, A. V.

APPLICANT: Kravchuk, L. L.

FILE OF INVENTION: In silico screening for phenotype-associated expressed sequence

CURRENT REFERENCE: 2760-103

CURRENT FILING DATE: 2002-05-30

NUMBER OF SEQ ID NOS: 415

SOFTWARE: PatentIn version 3.1

SEQ ID NO 341

LENGTH: 702

TYPE: PRT

ORGANISM: Homo sapiens

US-10-157-031-341

Query Match

Best Local Similarity 100.0%; Score 3721; DB 4; Length 702;

Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MESPSAPPHRCIPWQRLLLTASLLTFWNPPTAKLTIESTPRVAGKEVLLVHNPQ	60
DB	1	MESPSAPPHRCIPWQRLLLTASLLTFWNPPTAKLTIESTPRVAGKEVLLVHNPQ	60
QY	61	HLFYSYKGRVNDGNQIIGYVGTQATPGAPYSREIIPYASLLIIONIDNGFY	120
DB	61	HLFYSYKGRVNDGNQIIGYVGTQATPGAPYSREIIPYASLLIIONIDNGFY	120
QY	121	TLHVIKSDLVNEATGQFRYPPELKPSSISNNKPEVDKDAVAFTCEPETQATYLMV	180
DB	121	TLHVIKSDLVNEATGQFRYPPELKPSSISNNKPEVDKDAVAFTCEPETQATYLMV	180
QY	181	NNOSLPVSPRLQISNGRRTTLTFVNTNDTASVYCEFTONFVSARRSDSVILNLYGDPAP	240
DB	181	NNOSLPVSPRLQISNGRRTTLTFVNTNDTASVYCEFTONFVSARRSDSVILNLYGDPAP	240
QY	241	TISPLNTSYSGENLNSCHAAASNPAPQYMPFNGTQOSTOELFTINIVNNSGTYCQ	300
DB	241	TISPLNTSYSGENLNSCHAAASNPAPQYMPFNGTQOSTOELFTINIVNNSGTYCQ	300
QY	301	AHNSDTGLNRTVTTITVVAEPKPFITSNNSPVEDEDAVALTCEPEIONTTYLWVNN	360
DB	301	AHNSDTGLNRTVTTITVVAEPKPFITSNNSPVEDEDAVALTCEPEIONTTYLWVNN	360

QY 361 QSLPVSPRLQSLNDNRRTLLSVTRNDVGPYECGIONELSDVHSDPVLINLVLYGPDPTI 420
DB 361 QSLPVSPRLQSLNDNRRTLLSVTRNDVGPYECGIONELSDVHSDPVLINLVLYGPDPTI 420
QY 421 SPSTYYRPGVNLISCSHAASNPAPQYMWLDGNIQOHTQELFISNITEKNSGLYTCQAN 480
DB 421 SPSTYYRPGVNLISCSHAASNPAPQYMWLDGNIQOHTQELFISNITEKNSGLYTCQAN 480
QY 481 NSASGHSRTTYKTIIVSAELPKPSTISSNNSKPEVDKDAVAFCEPEAONTTYLMMVNGOS 540
DB 481 NSASGHSRTTYKTIIVSAELPKPSTISSNNSKPEVDKDAVAFCEPEAONTTYLMMVNGOS 540
QY 541 LPVSPRLQSLNDRRTLLFNTVRNDARAAYVCGIIONSVANSRSDPVTLDVLYGPDPTIISP 600
DB 541 LPVSPRLQSLNDRRTLLFNTVRNDARAAYVCGIIONSVANSRSDPVTLDVLYGPDPTIISP 600
QY 601 PSSSYLSGANLNLISCHASASNPSPQYSWRINGIPQOHTQVLFIAKTPNNNGTYACFVSNL 660
DB 601 PSSSYLSGANLNLISCHASASNPSPQYSWRINGIPQOHTQVLFIAKTPNNNGTYACFVSNL 660
QY 661 ATGRNNSIVKSTIVSASGTSPLSAGATVGMIGVLGVALLI 702
DB 661 ATGRNNSIVKSTIVSASGTSPLSAGATVGMIGVLGVALLI 702

RESULT 2

US-10-207-655-87
; Sequence 87, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069, 401C1
; CURRENT APPLICATION NUMBER: US/10/207, 655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 87
; LENGTH: 702
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-87

Query Match 100.0%; Score 3721; DB 4; Length 702;
Best Local Similarity 100.0%; Pred. No. 4, 5e-207; Indels 0; Gaps 0;
Matches 702; Conservative 0; Mismatches 0;
QY 1 MESPSAPPRHWCI PMORLLLTASLLTFMNPPTTAKLTISTEPFNAEGKEVLLVHNLPQ 60
DB 1 MESPSAPPRHWCI PMORLLLTASLLTFMNPPTTAKLTISTEPFNAEGKEVLLVHNLPQ 60
QY 61 HLFQYSWYGERVDGNRQIIGVYIGTOATPGPAYSGREIYFNASLLIQNIIONDTGEY 120
DB 61 HLFQYSWYGERVDGNRQIIGVYIGTOATPGPAYSGREIYFNASLLIQNIIONDTGEY 120
QY 121 TLHAVIKSDLVNEBATGQFRVYVPELPKPSISSNNSKPEVDKDAVAFCEPEAONTTYLMMV 180
DB 121 TLHAVIKSDLVNEBATGQFRVYVPELPKPSISSNNSKPEVDKDAVAFCEPEAONTTYLMMV 180
QY 181 NNQSLPVSPRLQSLNDRRTLLFNTVRNDARAAYVCGIIONSVANSRSDPVTLDVLYGPDAP 240
DB 181 NNQSLPVSPRLQSLNDRRTLLFNTVRNDARAAYVCGIIONSVANSRSDPVTLDVLYGPDAP 240
QY 241 TISPLNTSYRSGENLNLISCHASASNPAPQYSWFVNGTFQOSTOBLFIPNITVNNSGSYTCQ 300
DB 241 TISPLNTSYRSGENLNLISCHASASNPAPQYSWFVNGTFQOSTOBLFIPNITVNNSGSYTCQ 300
QY 301 AHNSDTGLRRTTYTITTYVAEPPKPTISNNSNPVDEDEVALTCPEIONTTYLMMVNN 360
DB 301 AHNSDTGLRRTTYTITTYVAEPPKPTISNNSNPVDEDEVALTCPEIONTTYLMMVNN 360
QY 361 QSLPVSPRLQSLNDNRRTLLSVTRNDVGPYECGIONELSDVHSDPVLINLVLYGPDPTI 420

DB 361 QSLPVSPRLQSLNDNRRTLLSVTRNDVGPYECGIONELSDVHSDPVLINLVLYGPDPTI 420
QY 421 SPSTYYRPGVNLISCSHAASNPAPQYMWLDGNIQOHTQELFISNITEKNSGLYTCQAN 480
DB 421 SPSTYYRPGVNLISCSHAASNPAPQYMWLDGNIQOHTQELFISNITEKNSGLYTCQAN 480
QY 481 NSASGHSRTTYKTIIVSAELPKPSTISSNNSKPEVDKDAVAFCEPEAONTTYLMMVNGOS 540
DB 481 NSASGHSRTTYKTIIVSAELPKPSTISSNNSKPEVDKDAVAFCEPEAONTTYLMMVNGOS 540
QY 541 LPVSPRLQSLNDRRTLLFNTVRNDARAAYVCGIIONSVANSRSDPVTLDVLYGPDPTIISP 600
DB 541 LPVSPRLQSLNDRRTLLFNTVRNDARAAYVCGIIONSVANSRSDPVTLDVLYGPDPTIISP 600
QY 601 PSSSYLSGANLNLISCHASASNPSPQYSWRINGIPQOHTQVLFIAKTPNNNGTYACFVSNL 660
DB 601 PSSSYLSGANLNLISCHASASNPSPQYSWRINGIPQOHTQVLFIAKTPNNNGTYACFVSNL 660
QY 661 ATGRNNSIVKSTIVSASGTSPLSAGATVGMIGVLGVALLI 702
DB 661 ATGRNNSIVKSTIVSASGTSPLSAGATVGMIGVLGVALLI 702

RESULT 3

US-10-117-937-592
; Sequence 592, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPILOPE SEQUENCES
; FILE REFERENCE: CTILIM, 027A
; CURRENT APPLICATION NUMBER: US/10/117, 937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282, 211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337, 017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363, 210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: PatSeq for Windows Version 4.0
; SEQ ID NO 592
; LENGTH: 702
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-592

Query Match 100.0%; Score 3721; DB 4; Length 702;
Best Local Similarity 100.0%; Pred. No. 4, 5e-207; Indels 0; Gaps 0;
Matches 702; Conservative 0; Mismatches 0;
QY 1 MESPSAPPRHWCI PMORLLLTASLLTFMNPPTTAKLTISTEPFNAEGKEVLLVHNLPQ 60
DB 1 MESPSAPPRHWCI PMORLLLTASLLTFMNPPTTAKLTISTEPFNAEGKEVLLVHNLPQ 60
QY 61 HLFQYSWYGERVDGNRQIIGVYIGTOATPGPAYSGREIYFNASLLIQNIIONDTGEY 120
DB 61 HLFQYSWYGERVDGNRQIIGVYIGTOATPGPAYSGREIYFNASLLIQNIIONDTGEY 120
QY 121 TLHAVIKSDLVNEBATGQFRVYVPELPKPSISSNNSKPEVDKDAVAFCEPEAONTTYLMMV 180
DB 121 TLHAVIKSDLVNEBATGQFRVYVPELPKPSISSNNSKPEVDKDAVAFCEPEAONTTYLMMV 180
QY 181 NNQSLPVSPRLQSLNDRRTLLFNTVRNDARAAYVCGIIONSVANSRSDPVTLDVLYGPDAP 240
DB 181 NNQSLPVSPRLQSLNDRRTLLFNTVRNDARAAYVCGIIONSVANSRSDPVTLDVLYGPDAP 240
QY 241 TISPLNTSYRSGENLNLISCHASASNPAPQYSWFVNGTFQOSTOBLFIPNITVNNSGSYTCQ 300

```

Db 241 TISPLNTSYRSGENLNLSCHSAASNPAPQSWFVNGTFOOSTOELFIPNITVNNSSGYTQ 300
Qy 301 AHNSDGTGNRTVTITTYAEPKPFITSNNSNPVEDDAVALTCEPEIONTTYLMMVNN 360
Db 301 AHNSDGTGNRTVTITTYAEPKPFITSNNSNPVEDDAVALTCEPEIONTTYLMMVNN 360
Qy 361 OSLPVSPRLQSLNDNRKTLTLFNTVRNDARAVYCGIIONSVSANSRSDPVTLDVLYGPDPTIIS 420
Db 361 OSLPVSPRLQSLNDNRKTLTLFNTVRNDARAVYCGIIONSVSANSRSDPVTLDVLYGPDPTI 420
Qy 421 SPSYTYRPGVNLISCHSAASNPAPQSWMLIDGNIQOHTOELFISNITEKNSGLTYTQAN 480
Db 421 SPSYTYRPGVNLISCHSAASNPAPQSWMLIDGNIQOHTOELFISNITEKNSGLTYTQAN 480
Qy 481 NSASGHSRTTYKTITVSABLPKPSISSNNSKVEDKDAVAFCEPEAONTTYLMMVNGOS 540
Db 481 NSASGHSRTTYKTITVSABLPKPSISSNNSKVEDKDAVAFCEPEAONTTYLMMVNGOS 540
Qy 541 LPVSPRLQSLNSGNRTLTLENTVRNDARAVYCGIIONSVSANSRSDPVTLDVLYGPDPTIIS 600
Db 541 LPVSPRLQSLNSGNRTLTLENTVRNDARAVYCGIIONSVSANSRSDPVTLDVLYGPDPTIIS 600
Qy 601 PDSSYLSGANLNLSCHSAASNPAPQSWRINGIPQOHTOELFIAKITPNNNGTYACFVSNTL 660
Db 601 PDSSYLSGANLNLSCHSAASNPAPQSWRINGIPQOHTOELFIAKITPNNNGTYACFVSNTL 660
Qy 661 ATGRNNSIVKSIITVSASGTSFGLSAGATVGMIGLVGVALI 702
Db 661 ATGRNNSIVKSIITVSASGTSFGLSAGATVGMIGLVGVALI 702

```

RESULT 4

```

US-10-295-027-332
; Sequence 332, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Gineberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezl, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.

```

```

; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 332
; LENGTH: 702
; TYPE: PR
; ORGANISM: Homo sapiens
US-10-295-027-332

```

```

Query Match 100.0%; Score 3721; DB 4; Length 702;
Best Local Similarity 100.0%; Pred.No. 4.5e-207;
Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 MESPSAPPRKWCIPQORLLTASLTLENNPPTAKLTISTEPNNVAGKGVLLVNNLPQ 60
Db 1 MESPSAPPRKWCIPQORLLTASLTLENNPPTAKLTISTEPNNVAGKGVLLVNNLPQ 60
Qy 61 HLFQSWYKGERVDGNRQIIGYVIGTQOATPGPAYSGBREIIPNASLLIIONIIQNDTGFY 120
Db 61 HLFQSWYKGERVDGNRQIIGYVIGTQOATPGPAYSGBREIIPNASLLIIONIIQNDTGFY 120
Qy 121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKVEDKDAVAFCEPEAONTTYLMMV 180
Db 121 TLHVIKSDLVNEEATGQFRVYPELPKPSISSNNSKVEDKDAVAFCEPEAONTTYLMMV 180
Qy 181 NNQSLPVSPRLQSLNSGNRTLTLENTVRNDARAVYCGIIONSVSANSRSDPVTLDVLYGPDAP 240
Db 181 NNQSLPVSPRLQSLNSGNRTLTLENTVRNDARAVYCGIIONSVSANSRSDPVTLDVLYGPDAP 240
Qy 241 TISPLNTSYRSGENLNLSCHSAASNPAPQSWFVNGTFOOSTOELFIPNITVNNSSGYTQ 300
Db 241 TISPLNTSYRSGENLNLSCHSAASNPAPQSWFVNGTFOOSTOELFIPNITVNNSSGYTQ 300
Qy 301 AHNSDGTGNRTVTITTYAEPKPFITSNNSNPVEDDAVALTCEPEIONTTYLMMVNN 360
Db 301 AHNSDGTGNRTVTITTYAEPKPFITSNNSNPVEDDAVALTCEPEIONTTYLMMVNN 360
Qy 361 OSLPVSPRLQSLNDNRKTLTLFNTVRNDARAVYCGIIONSVSANSRSDPVTLDVLYGPDPTI 420
Db 361 OSLPVSPRLQSLNDNRKTLTLFNTVRNDARAVYCGIIONSVSANSRSDPVTLDVLYGPDPTI 420
Qy 421 SPSYTYRPGVNLISCHSAASNPAPQSWMLIDGNIQOHTOELFISNITEKNSGLTYTQAN 480
Db 421 SPSYTYRPGVNLISCHSAASNPAPQSWMLIDGNIQOHTOELFISNITEKNSGLTYTQAN 480
Qy 481 NSASGHSRTTYKTITVSABLPKPSISSNNSKVEDKDAVAFCEPEAONTTYLMMVNGOS 540
Db 481 NSASGHSRTTYKTITVSABLPKPSISSNNSKVEDKDAVAFCEPEAONTTYLMMVNGOS 540
Qy 541 LPVSPRLQSLNSGNRTLTLENTVRNDARAVYCGIIONSVSANSRSDPVTLDVLYGPDPTIIS 600
Db 541 LPVSPRLQSLNSGNRTLTLENTVRNDARAVYCGIIONSVSANSRSDPVTLDVLYGPDPTIIS 600
Qy 601 PDSSYLSGANLNLSCHSAASNPAPQSWRINGIPQOHTOELFIAKITPNNNGTYACFVSNTL 660
Db 601 PDSSYLSGANLNLSCHSAASNPAPQSWRINGIPQOHTOELFIAKITPNNNGTYACFVSNTL 660
Qy 661 ATGRNNSIVKSIITVSASGTSFGLSAGATVGMIGLVGVALI 702
Db 661 ATGRNNSIVKSIITVSASGTSFGLSAGATVGMIGLVGVALI 702

```

RESULT 5

```

US-10-245-871-282
; Sequence 282, Application US/10245871
; Publication No. US20030235594A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: II-KEY/ANTIGENIC EPTOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2013
; CURRENT APPLICATION NUMBER: US/10/245,871
; CURRENT FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: 10/197,000

```

;
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 905
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 282
; LENGTH: 702
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-245-871-282

Query Match 100.0%; Score 3721; DB 4; Length 702;
Best Local Similarity 100.0%; Pred. No. 4.5e-207;
Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESPSAPPHRMCI PMQRLTLTSLTFMNPPTAKLTISTEPNVAEGKVLVHNL PQ 60
DB 1 MESPSAPPHRMCI PMQRLTLTSLTFMNPPTAKLTISTEPNVAEGKVLVHNL PQ 60
QY 61 HLFQSWYKGERVDGNRQIIIGVIGTQATPGPAYSGREIIPNASLLIQNIIONDTGFX 120
DB 61 HLFQSWYKGERVDGNRQIIIGVIGTQATPGPAYSGREIIPNASLLIQNIIONDTGFX 120
QY 121 TLHVIKSDLVNEBAGQFRVYPELPKPSISSNSKPEVEDKDAVAFCEPETQDATYLMVY 180
DB 121 TLHVIKSDLVNEBAGQFRVYPELPKPSISSNSKPEVEDKDAVAFCEPETQDATYLMVY 180
QY 181 NNQSLPVSPRLQLSNGNRRLTLFNVTRNDTASKYCETONPVARSDSVILNVL YGPDAP 240
DB 181 NNQSLPVSPRLQLSNGNRRLTLFNVTRNDTASKYCETONPVARSDSVILNVL YGPDAP 240
QY 241 TISPLNTSYRSGENLNLSCHAASNPPAOYSWFVNGTFQOSTOELFIPNITVNNSSGYTCQ 300
DB 241 TISPLNTSYRSGENLNLSCHAASNPPAOYSWFVNGTFQOSTOELFIPNITVNNSSGYTCQ 300
QY 301 AHNSTDGLNRRTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLMMVNN 360
DB 301 AHNSTDGLNRRTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLMMVNN 360
QY 361 QSLPVSPRLQLSNDNRRLTLTSLTRNDVGPYECGIONELSVHSDPVLNVL YGPDPT 420
DB 361 QSLPVSPRLQLSNDNRRLTLTSLTRNDVGPYECGIONELSVHSDPVLNVL YGPDPT 420
QY 421 SPSTYTYRPGVNLSLSCHAASNPPAOYSWLDIGNIOHTOELFISNITERKNSGLYTCQAN 480
DB 421 SPSTYTYRPGVNLSLSCHAASNPPAOYSWLDIGNIOHTOELFISNITERKNSGLYTCQAN 480
QY 481 NSASGHSRTTVKTTIVSAELPKPSISSNSKPEVEDKDAVAFCEPEAQNTTYLMMVNGOS 540
DB 481 NSASGHSRTTVKTTIVSAELPKPSISSNSKPEVEDKDAVAFCEPEAQNTTYLMMVNGOS 540
QY 541 LPPVSPRLQLSNGNRRLTLFNVTRNDARAYVCGIONSVSANRSDPYTLNVL YGPDPTIISP 600
DB 541 LPPVSPRLQLSNGNRRLTLFNVTRNDARAYVCGIONSVSANRSDPYTLNVL YGPDPTIISP 600
QY 601 PDSSYLSGANLNLSCHASNPSPQYSWRINGIPQOHTOVLFLAKITPPNNGTYACFVSNL 660
DB 601 PDSSYLSGANLNLSCHASNPSPQYSWRINGIPQOHTOVLFLAKITPPNNGTYACFVSNL 660
QY 661 ATGRNNSIVKSTIVSASGTS PGLSAGATVIGIMIGLVGVALI 702
DB 661 ATGRNNSIVKSTIVSASGTS PGLSAGATVIGIMIGLVGVALI 702

RESULT 6
US-10-253-286-282

; Sequence 282, Application US/10253286
; Publication No. US20040058881A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: II-KEY/ANTIGENIC EPTOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2015

;
; CURRENT APPLICATION NUMBER: US/10/253,286
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 905
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 282
; LENGTH: 702
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-253-286-282

Query Match 100.0%; Score 3721; DB 4; Length 702;
Best Local Similarity 100.0%; Pred. No. 4.5e-207;
Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESPSAPPHRMCI PMQRLTLTSLTFMNPPTAKLTISTEPNVAEGKVLVHNL PQ 60
DB 1 MESPSAPPHRMCI PMQRLTLTSLTFMNPPTAKLTISTEPNVAEGKVLVHNL PQ 60
QY 61 HLFQSWYKGERVDGNRQIIIGVIGTQATPGPAYSGREIIPNASLLIQNIIONDTGFX 120
DB 61 HLFQSWYKGERVDGNRQIIIGVIGTQATPGPAYSGREIIPNASLLIQNIIONDTGFX 120
QY 121 TLHVIKSDLVNEBAGQFRVYPELPKPSISSNSKPEVEDKDAVAFCEPETQDATYLMVY 180
DB 121 TLHVIKSDLVNEBAGQFRVYPELPKPSISSNSKPEVEDKDAVAFCEPETQDATYLMVY 180
QY 181 NNQSLPVSPRLQLSNGNRRLTLFNVTRNDTASKYCETONPVARSDSVILNVL YGPDAP 240
DB 181 NNQSLPVSPRLQLSNGNRRLTLFNVTRNDTASKYCETONPVARSDSVILNVL YGPDAP 240
QY 241 TISPLNTSYRSGENLNLSCHAASNPPAOYSWFVNGTFQOSTOELFIPNITVNNSSGYTCQ 300
DB 241 TISPLNTSYRSGENLNLSCHAASNPPAOYSWFVNGTFQOSTOELFIPNITVNNSSGYTCQ 300
QY 301 AHNSTDGLNRRTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLMMVNN 360
DB 301 AHNSTDGLNRRTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLMMVNN 360
QY 361 QSLPVSPRLQLSNDNRRLTLTSLTRNDVGPYECGIONELSVHSDPVLNVL YGPDPT 420
DB 361 QSLPVSPRLQLSNDNRRLTLTSLTRNDVGPYECGIONELSVHSDPVLNVL YGPDPT 420
QY 421 SPSTYTYRPGVNLSLSCHAASNPPAOYSWLDIGNIOHTOELFISNITERKNSGLYTCQAN 480
DB 421 SPSTYTYRPGVNLSLSCHAASNPPAOYSWLDIGNIOHTOELFISNITERKNSGLYTCQAN 480
QY 481 NSASGHSRTTVKTTIVSAELPKPSISSNSKPEVEDKDAVAFCEPEAQNTTYLMMVNGOS 540
DB 481 NSASGHSRTTVKTTIVSAELPKPSISSNSKPEVEDKDAVAFCEPEAQNTTYLMMVNGOS 540
QY 541 LPPVSPRLQLSNGNRRLTLFNVTRNDARAYVCGIONSVSANRSDPYTLNVL YGPDPTIISP 600
DB 541 LPPVSPRLQLSNGNRRLTLFNVTRNDARAYVCGIONSVSANRSDPYTLNVL YGPDPTIISP 600
QY 601 PDSSYLSGANLNLSCHASNPSPQYSWRINGIPQOHTOVLFLAKITPPNNGTYACFVSNL 660
DB 601 PDSSYLSGANLNLSCHASNPSPQYSWRINGIPQOHTOVLFLAKITPPNNGTYACFVSNL 660
QY 661 ATGRNNSIVKSTIVSASGTS PGLSAGATVIGIMIGLVGVALI 702
DB 661 ATGRNNSIVKSTIVSASGTS PGLSAGATVIGIMIGLVGVALI 702

RESULT 7
US-10-380-136-16

; Sequence 16, Application US/10380136
; Publication No. US20040071726A1
; GENERAL INFORMATION:
; APPLICANT: Chicz, Roman M.

APPLICANT: Tomlinson, Andy
TITLE OF INVENTION: PEPTIDE RINOPES RECOGNIZED BY ANTIGEN
FILE OF INVENTION: SPECIFIC CDA+ T LYMPHOCYTES
FILE REFERENCE: 08191-019051
CURRENT APPLICATION NUMBER: US/10/380,136
CURRENT FILING DATE: 2003-03-11
PRIOR APPLICATION NUMBER: PCT/US01/28467
PRIOR FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: US 60/232,185
PRIOR FILING DATE: 2000-09-12
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16
LENGTH: 702
TYPE: PRT
ORGANISM: Homo sapiens
US-10-380-136-16

Query Match 100.0%; Score 3721; DB 4; Length 702;
Best Local Similarity 100.0%; Pred. No. 4.5e-207;
Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESBPAPHRMCI PWQRLLLTASLTFTFNPPPTAKLTTESTPNNVAGKEVLLVHNLPO 60
DB 1 MESBPAPHRMCI PWQRLLLTASLTFTFNPPPTAKLTTESTPNNVAGKEVLLVHNLPO 60
QY 61 HLFQSWYKGERVDGNROIIIGVIGTOATPGPAYSGREIIPNASSLIIQNIIONDTGFX 120
DB 61 HLFQSWYKGERVDGNROIIIGVIGTOATPGPAYSGREIIPNASSLIIQNIIONDTGFX 120
QY 121 TLHVIKSDLVNEBAGQFRVYVPELPKPSISSNNSKPVEDKDAVAFTCEBETODATYLMWV 180
DB 121 TLHVIKSDLVNEBAGQFRVYVPELPKPSISSNNSKPVEDKDAVAFTCEBETODATYLMWV 180
QY 181 NNQSLPVSPRLQSLSGNRTLTLLFNTRNDTASYKETONPVARSDSYILNVLGPDAP 240
DB 181 NNQSLPVSPRLQSLSGNRTLTLLFNTRNDTASYKETONPVARSDSYILNVLGPDAP 240
QY 241 TISPLNTSYRSGENINLSCHASNPAPQYSWFVNGTFQOSTOELFIPNITVNNSSGYTCQ 300
DB 241 TISPLNTSYRSGENINLSCHASNPAPQYSWFVNGTFQOSTOELFIPNITVNNSSGYTCQ 300
QY 301 AHSNPDGLNRTTITVYVAPPKPFISSNNSNPVEDDAVALTCEPEIQTNTYLMWVN 360
DB 301 AHSNPDGLNRTTITVYVAPPKPFISSNNSNPVEDDAVALTCEPEIQTNTYLMWVN 360
QY 361 QSLPVSPRLQSLSGNRTLTLLSVTRNDVGPYECGIONELSDHSDPVILNVLGPDPTI 420
DB 361 QSLPVSPRLQSLSGNRTLTLLSVTRNDVGPYECGIONELSDHSDPVILNVLGPDPTI 420
QY 421 SPSTYYRPGVNLISCHASNPAPQYSWMLIDGNIQOHTOELFISNTERKSGLYTQAN 480
DB 421 SPSTYYRPGVNLISCHASNPAPQYSWMLIDGNIQOHTOELFISNTERKSGLYTQAN 480
QY 481 NSASGHSRTTYKTTIVSAELPKPSISSNNSKPVEDKDAVAFTCEBEAONTTYLMWVNSQS 540
DB 481 NSASGHSRTTYKTTIVSAELPKPSISSNNSKPVEDKDAVAFTCEBEAONTTYLMWVNSQS 540
QY 541 LPVSPRLQSLSGNRTLTLLFNTRNDARAYVCGIQNSVANSDPVTLLVLYGPDPTIISP 600
DB 541 LPVSPRLQSLSGNRTLTLLFNTRNDARAYVCGIQNSVANSDPVTLLVLYGPDPTIISP 600
QY 601 PDSSYLSGANINLSCHASNPSPQYSWRINGIPOOHTOVLFIAKTPNNGTYACFVSNL 660
DB 601 PDSSYLSGANINLSCHASNPSPQYSWRINGIPOOHTOVLFIAKTPNNGTYACFVSNL 660
QY 661 ATGRNNSIVKSIITVSAAGTSPGLSAGATVGMIGLVGVALI 702
DB 661 ATGRNNSIVKSIITVSAAGTSPGLSAGATVGMIGLVGVALI 702

RESULT 8
US-10-149-137A-458

Sequence 458, Application US/10149137A
Publication No. US20040146519A1
GENERAL INFORMATION:
APPLICANT: Fikes, John
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Cella, Esteban
APPLICANT: Keogh, Elissa
TITLE OF INVENTION: Inducing Cellular Immune Responses to Carcinoma/embryonic
FILE OF INVENTION: Antigen Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.008006
CURRENT APPLICATION NUMBER: US/10/149,137A
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: PCT/US00/33574
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 09/458,302
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 562
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 458
LENGTH: 702
TYPE: PRT
ORGANISM: Homo sapiens
US-10-149-137A-458

Query Match 100.0%; Score 3721; DB 4; Length 702;
Best Local Similarity 100.0%; Pred. No. 4.5e-207;
Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESBPAPHRMCI PWQRLLLTASLTFTFNPPPTAKLTTESTPNNVAGKEVLLVHNLPO 60
DB 1 MESBPAPHRMCI PWQRLLLTASLTFTFNPPPTAKLTTESTPNNVAGKEVLLVHNLPO 60
QY 61 HLFQSWYKGERVDGNROIIIGVIGTOATPGPAYSGREIIPNASSLIIQNIIONDTGFX 120
DB 61 HLFQSWYKGERVDGNROIIIGVIGTOATPGPAYSGREIIPNASSLIIQNIIONDTGFX 120
QY 121 TLHVIKSDLVNEBAGQFRVYVPELPKPSISSNNSKPVEDKDAVAFTCEBETODATYLMWV 180
DB 121 TLHVIKSDLVNEBAGQFRVYVPELPKPSISSNNSKPVEDKDAVAFTCEBETODATYLMWV 180
QY 181 NNQSLPVSPRLQSLSGNRTLTLLFNTRNDTASYKETONPVARSDSYILNVLGPDAP 240
DB 181 NNQSLPVSPRLQSLSGNRTLTLLFNTRNDTASYKETONPVARSDSYILNVLGPDAP 240
QY 241 TISPLNTSYRSGENINLSCHASNPAPQYSWFVNGTFQOSTOELFIPNITVNNSSGYTCQ 300
DB 241 TISPLNTSYRSGENINLSCHASNPAPQYSWFVNGTFQOSTOELFIPNITVNNSSGYTCQ 300
QY 301 AHSNPDGLNRTTITVYVAPPKPFISSNNSNPVEDDAVALTCEPEIQTNTYLMWVN 360
DB 301 AHSNPDGLNRTTITVYVAPPKPFISSNNSNPVEDDAVALTCEPEIQTNTYLMWVN 360
QY 361 QSLPVSPRLQSLSGNRTLTLLSVTRNDVGPYECGIONELSDHSDPVILNVLGPDPTI 420
DB 361 QSLPVSPRLQSLSGNRTLTLLSVTRNDVGPYECGIONELSDHSDPVILNVLGPDPTI 420
QY 421 SPSTYYRPGVNLISCHASNPAPQYSWMLIDGNIQOHTOELFISNTERKSGLYTQAN 480
DB 421 SPSTYYRPGVNLISCHASNPAPQYSWMLIDGNIQOHTOELFISNTERKSGLYTQAN 480
QY 481 NSASGHSRTTYKTTIVSAELPKPSISSNNSKPVEDKDAVAFTCEBEAONTTYLMWVNSQS 540
DB 481 NSASGHSRTTYKTTIVSAELPKPSISSNNSKPVEDKDAVAFTCEBEAONTTYLMWVNSQS 540
QY 541 LPVSPRLQSLSGNRTLTLLFNTRNDARAYVCGIQNSVANSDPVTLLVLYGPDPTIISP 600
DB 541 LPVSPRLQSLSGNRTLTLLFNTRNDARAYVCGIQNSVANSDPVTLLVLYGPDPTIISP 600
QY 601 PDSSYLSGANINLSCHASNPSPQYSWRINGIPOOHTOVLFIAKTPNNGTYACFVSNL 660
DB 601 PDSSYLSGANINLSCHASNPSPQYSWRINGIPOOHTOVLFIAKTPNNGTYACFVSNL 660

Db 601 PSSSYLGANLNLSCHASNPSPQYSWRINGIPQOHTOVLFAKITTNNNGTYACFVSNL 660
QY 661 ATGRNNSIVKSIITVSASGTSPLSAGATYGMIGVLVGVALLI 702
Db 661 ATGRNNSIVKSIITVSASGTSPLSAGATYGMIGVLVGVALLI 702

RESULT 9
US-10-712-124-74
; Sequence 74, Application US/10712124
; Publication No. US20040146907A1
; GENERAL INFORMATION:
; APPLICANT: SMITH, VICTORIA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING DYSPLASIA
; FILE REFERENCE: P2000R1
; CURRENT APPLICATION NUMBER: US/10/712,124
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/425,813
; NUMBER OF SEQ ID NOS: 123
; SEQ ID NO 74
; LENGTH: 702
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-712-124-74

Query Match 100.0%; Score 3721; DB 4; Length 702;
Best Local Similarity 100.0%; Pred. No. 4.5e-207;
Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESPSAPPHRMCIIPWQRLTLTASLTFPMNPPTAKLTISTEPFNAEGKEVLLVHNLPQ 60
Db 1 MESPSAPPHRMCIIPWQRLTLTASLTFPMNPPTAKLTISTEPFNAEGKEVLLVHNLPQ 60
QY 61 HLFEGSWYGERVDGNRQIIGYVIGTQOATPGPAYSGREIIPNASLLIQNIIONDTGFI 120
Db 61 HLFEGSWYGERVDGNRQIIGYVIGTQOATPGPAYSGREIIPNASLLIQNIIONDTGFI 120
QY 121 TLHVIKSDLVNEBATOQFVRYPELPKPSISSNNSKXVEDKDAVAFCEPETODATYLMVY 180
Db 121 TLHVIKSDLVNEBATOQFVRYPELPKPSISSNNSKXVEDKDAVAFCEPETODATYLMVY 180
QY 181 NNQSLPVSRLQLSNGNRRLTLFNVTRNDTASYKCETONPVARSDSVILNVLVGPDPAP 240
Db 181 NNQSLPVSRLQLSNGNRRLTLFNVTRNDTASYKCETONPVARSDSVILNVLVGPDPAP 240
QY 241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWPNVNGTFQOSTOELFIPNITVNNSGSYTCQ 300
Db 241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWPNVNGTFQOSTOELFIPNITVNNSGSYTCQ 300
QY 301 AHNSDTGLNRRTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLMMVNN 360
Db 301 AHNSDTGLNRRTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLMMVNN 360
QY 361 QSLPVSRLQLSNDNRRLTLFNVTRNDVGPYECGIONELSVHSDPVLINVLVGPDDPTI 420
Db 361 QSLPVSRLQLSNDNRRLTLFNVTRNDVGPYECGIONELSVHSDPVLINVLVGPDDPTI 420
QY 421 SPSTYTYRGGVNLISCHASNPAPQYSWIDGNIOQHOLEFISNTEKNSGLYTCQAN 480
Db 421 SPSTYTYRGGVNLISCHASNPAPQYSWIDGNIOQHOLEFISNTEKNSGLYTCQAN 480
QY 481 NSASGHSRTTVKTIITVSASLPPKPSISSNNSKXVEDKDAVAFCEPEAQNTTYLMMVNGOS 540
Db 481 NSASGHSRTTVKTIITVSASLPPKPSISSNNSKXVEDKDAVAFCEPEAQNTTYLMMVNGOS 540
QY 541 LVPSPRLQLSNGNRRLTLFNVTRNDARAAYCGIQNSVSANRSDPVTLDVLVGPDPPIISP 600
Db 541 LVPSPRLQLSNGNRRLTLFNVTRNDARAAYCGIQNSVSANRSDPVTLDVLVGPDPPIISP 600
QY 601 PSSSYLGANLNLSCHASNPSPQYSWRINGIPQOHTOVLFAKITTNNNGTYACFVSNL 660
Db 601 PSSSYLGANLNLSCHASNPSPQYSWRINGIPQOHTOVLFAKITTNNNGTYACFVSNL 660

RESULT 10
US-10-734-564-72
; Sequence 72, Application US/10734564
; Publication No. US20040157278A1
; GENERAL INFORMATION:
; APPLICANT: Christopher C Burgess et al
; TITLE OF INVENTION: Detection Methods Using T1MP1
; FILE REFERENCE: 1657/2012
; CURRENT APPLICATION NUMBER: US/10/734,564
; PRIOR FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 702
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-734-564-72

Query Match 100.0%; Score 3721; DB 4; Length 702;
Best Local Similarity 100.0%; Pred. No. 4.5e-207;
Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESPSAPPHRMCIIPWQRLTLTASLTFPMNPPTAKLTISTEPFNAEGKEVLLVHNLPQ 60
Db 1 MESPSAPPHRMCIIPWQRLTLTASLTFPMNPPTAKLTISTEPFNAEGKEVLLVHNLPQ 60
QY 61 HLFEGSWYGERVDGNRQIIGYVIGTQOATPGPAYSGREIIPNASLLIQNIIONDTGFI 120
Db 61 HLFEGSWYGERVDGNRQIIGYVIGTQOATPGPAYSGREIIPNASLLIQNIIONDTGFI 120
QY 121 TLHVIKSDLVNEBATOQFVRYPELPKPSISSNNSKXVEDKDAVAFCEPETODATYLMVY 180
Db 121 TLHVIKSDLVNEBATOQFVRYPELPKPSISSNNSKXVEDKDAVAFCEPETODATYLMVY 180
QY 181 NNQSLPVSRLQLSNGNRRLTLFNVTRNDTASYKCETONPVARSDSVILNVLVGPDPAP 240
Db 181 NNQSLPVSRLQLSNGNRRLTLFNVTRNDTASYKCETONPVARSDSVILNVLVGPDPAP 240
QY 241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWPNVNGTFQOSTOELFIPNITVNNSGSYTCQ 300
Db 241 TISPLNTSYRSGENLNLSCHAASNPPAQYSWPNVNGTFQOSTOELFIPNITVNNSGSYTCQ 300
QY 301 AHNSDTGLNRRTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLMMVNN 360
Db 301 AHNSDTGLNRRTVTTITVYAEPPKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLMMVNN 360
QY 361 QSLPVSRLQLSNDNRRLTLFNVTRNDVGPYECGIONELSVHSDPVLINVLVGPDDPTI 420
Db 361 QSLPVSRLQLSNDNRRLTLFNVTRNDVGPYECGIONELSVHSDPVLINVLVGPDDPTI 420
QY 421 SPSTYTYRGGVNLISCHASNPAPQYSWIDGNIOQHOLEFISNTEKNSGLYTCQAN 480
Db 421 SPSTYTYRGGVNLISCHASNPAPQYSWIDGNIOQHOLEFISNTEKNSGLYTCQAN 480
QY 481 NSASGHSRTTVKTIITVSASLPPKPSISSNNSKXVEDKDAVAFCEPEAQNTTYLMMVNGOS 540
Db 481 NSASGHSRTTVKTIITVSASLPPKPSISSNNSKXVEDKDAVAFCEPEAQNTTYLMMVNGOS 540
QY 541 LVPSPRLQLSNGNRRLTLFNVTRNDARAAYCGIQNSVSANRSDPVTLDVLVGPDPPIISP 600
Db 541 LVPSPRLQLSNGNRRLTLFNVTRNDARAAYCGIQNSVSANRSDPVTLDVLVGPDPPIISP 600
QY 601 PSSSYLGANLNLSCHASNPSPQYSWRINGIPQOHTOVLFAKITTNNNGTYACFVSNL 660
Db 601 PSSSYLGANLNLSCHASNPSPQYSWRINGIPQOHTOVLFAKITTNNNGTYACFVSNL 660
QY 661 ATGRNNSIVKSIITVSASGTSPLSAGATYGMIGVLVGVALLI 702

Db 661 ATGRNNSIVKSTTVASAGTSPGLSAGATGIMIGLVGVALL 702

RESULT 11
US-10-657-022-88
; Sequence 88, Application US/10657022
; Publication No. US20040180354A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Liu, Zheng
; APPLICANT: Liu, Zheng
; TITLE OF INVENTION: EPILOPE SEQUENCES
; FILE REFERENCE: MANUK 032A
; CURRENT APPLICATION NUMBER: US/10/657,022
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: 60/409123
; PRIOR FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 610
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 702
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-657-022-88

Query Match 100.0%; Score 3721; DB 4; Length 702;
Best Local Similarity 100.0%; Pred. No. 4.5e-207;
Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MESBPAPHRMCIPQORLLTASLLTFNNPPTAKLTTESTPBNVABGEVLLVHNPQ 60
Db 1 MESBPAPHRMCIPQORLLTASLLTFNNPPTAKLTTESTPBNVABGEVLLVHNPQ 60

Qy 61 HLFQSWYKGRVDGNRQIIIGVIGTQOATPGPAYSGREIIPNASSLIQNIQNDTGFY 120
Db 61 HLFQSWYKGRVDGNRQIIIGVIGTQOATPGPAYSGREIIPNASSLIQNIQNDTGFY 120

Qy 121 TLHVIKSDLVNEBATGQFRVYBELPKPSISSNNSKPVEDKDAVAFTCEPETODATYLMWV 180
Db 121 TLHVIKSDLVNEBATGQFRVYBELPKPSISSNNSKPVEDKDAVAFTCEPETODATYLMWV 180

Qy 121 TLHVIKSDLVNEBATGQFRVYBELPKPSISSNNSKPVEDKDAVAFTCEPETODATYLMWV 180
Db 121 TLHVIKSDLVNEBATGQFRVYBELPKPSISSNNSKPVEDKDAVAFTCEPETODATYLMWV 180

Qy 181 NNOSLPVSPRLOLSNGNRTTLTFNTRNDTASYKETONPVSARSDSVILNLVYGPAP 240
Db 181 NNOSLPVSPRLOLSNGNRTTLTFNTRNDTASYKETONPVSARSDSVILNLVYGPAP 240

Qy 241 TISPLNTSYRSGENMLNSCHASNPAPQYSWFVNGTFOOSTOELFIPNITVNNSGSYTCQ 300
Db 241 TISPLNTSYRSGENMLNSCHASNPAPQYSWFVNGTFOOSTOELFIPNITVNNSGSYTCQ 300

Qy 241 TISPLNTSYRSGENMLNSCHASNPAPQYSWFVNGTFOOSTOELFIPNITVNNSGSYTCQ 300
Db 241 TISPLNTSYRSGENMLNSCHASNPAPQYSWFVNGTFOOSTOELFIPNITVNNSGSYTCQ 300

Qy 301 AHSNDTGLNRTTYYTITVYAPPKPFTSSNNSNPEVEDDAVALTCEPEIQNTTYLMMVNN 360
Db 301 AHSNDTGLNRTTYYTITVYAPPKPFTSSNNSNPEVEDDAVALTCEPEIQNTTYLMMVNN 360

Qy 301 AHSNDTGLNRTTYYTITVYAPPKPFTSSNNSNPEVEDDAVALTCEPEIQNTTYLMMVNN 360
Db 301 AHSNDTGLNRTTYYTITVYAPPKPFTSSNNSNPEVEDDAVALTCEPEIQNTTYLMMVNN 360

Qy 361 OSLSVSPRLOLSNGNRTTLTSLVTRNDVGPKECGIQNELSDVHSDPVILNLVYGPDDPTI 420
Db 361 OSLSVSPRLOLSNGNRTTLTSLVTRNDVGPKECGIQNELSDVHSDPVILNLVYGPDDPTI 420

Qy 361 OSLSVSPRLOLSNGNRTTLTSLVTRNDVGPKECGIQNELSDVHSDPVILNLVYGPDDPTI 420
Db 361 OSLSVSPRLOLSNGNRTTLTSLVTRNDVGPKECGIQNELSDVHSDPVILNLVYGPDDPTI 420

Qy 421 SPSYTYRPGVNLISLCHASNPAPQYSWMLIDGNIQOHTOELFISNITEKNSGLYTQCAN 480
Db 421 SPSYTYRPGVNLISLCHASNPAPQYSWMLIDGNIQOHTOELFISNITEKNSGLYTQCAN 480

Qy 421 SPSYTYRPGVNLISLCHASNPAPQYSWMLIDGNIQOHTOELFISNITEKNSGLYTQCAN 480
Db 421 SPSYTYRPGVNLISLCHASNPAPQYSWMLIDGNIQOHTOELFISNITEKNSGLYTQCAN 480

Qy 481 NSASGHSRTTYKTTIVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLMMVNNQS 540
Db 481 NSASGHSRTTYKTTIVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLMMVNNQS 540

Qy 481 NSASGHSRTTYKTTIVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLMMVNNQS 540
Db 481 NSASGHSRTTYKTTIVSAELPKPSISSNNSKPVEDKDAVAFTCEPEAQNTTYLMMVNNQS 540

Qy 541 LPVSPRLOLSNGNRTTLTFNTRNDARAYVCGIQNSVANSRSDPTLVLVYGPDDPTI 600
Db 541 LPVSPRLOLSNGNRTTLTFNTRNDARAYVCGIQNSVANSRSDPTLVLVYGPDDPTI 600

Qy 541 LPVSPRLOLSNGNRTTLTFNTRNDARAYVCGIQNSVANSRSDPTLVLVYGPDDPTI 600
Db 541 LPVSPRLOLSNGNRTTLTFNTRNDARAYVCGIQNSVANSRSDPTLVLVYGPDDPTI 600

Qy 601 PDSSYLSGANLNLSCHASNPSPQYSWRINGIPOOHTOVLFLAKITPNNNGTYACFVSNL 660
Db 601 PDSSYLSGANLNLSCHASNPSPQYSWRINGIPOOHTOVLFLAKITPNNNGTYACFVSNL 660

Db 601 PDSSYLSGANLNLSCHASNPSPQYSWRINGIPOOHTOVLFLAKITPNNNGTYACFVSNL 660

Qy 661 ATGRNNSIVKSTTVASAGTSPGLSAGATGIMIGLVGVALL 702

Db 661 ATGRNNSIVKSTTVASAGTSPGLSAGATGIMIGLVGVALL 702

RESULT 12
US-10-473-127-1462
; Sequence 1462, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1462
; LENGTH: 702
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1462

Query Match 100.0%; Score 3721; DB 5; Length 702;
Best Local Similarity 100.0%; Pred. No. 4.5e-207;
Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MESBPAPHRMCIPQORLLTASLLTFNNPPTAKLTTESTPBNVABGEVLLVHNPQ 60
Db 1 MESBPAPHRMCIPQORLLTASLLTFNNPPTAKLTTESTPBNVABGEVLLVHNPQ 60

Qy 61 HLFQSWYKGRVDGNRQIIIGVIGTQOATPGPAYSGREIIPNASSLIQNIQNDTGFY 120
Db 61 HLFQSWYKGRVDGNRQIIIGVIGTQOATPGPAYSGREIIPNASSLIQNIQNDTGFY 120

Qy 121 TLHVIKSDLVNEBATGQFRVYBELPKPSISSNNSKPVEDKDAVAFTCEPETODATYLMWV 180
Db 121 TLHVIKSDLVNEBATGQFRVYBELPKPSISSNNSKPVEDKDAVAFTCEPETODATYLMWV 180

Qy 121 TLHVIKSDLVNEBATGQFRVYBELPKPSISSNNSKPVEDKDAVAFTCEPETODATYLMWV 180
Db 121 TLHVIKSDLVNEBATGQFRVYBELPKPSISSNNSKPVEDKDAVAFTCEPETODATYLMWV 180

Qy 181 NNOSLPVSPRLOLSNGNRTTLTFNTRNDTASYKETONPVSARSDSVILNLVYGPAP 240
Db 181 NNOSLPVSPRLOLSNGNRTTLTFNTRNDTASYKETONPVSARSDSVILNLVYGPAP 240

Qy 181 NNOSLPVSPRLOLSNGNRTTLTFNTRNDTASYKETONPVSARSDSVILNLVYGPAP 240
Db 181 NNOSLPVSPRLOLSNGNRTTLTFNTRNDTASYKETONPVSARSDSVILNLVYGPAP 240

Qy 241 TISPLNTSYRSGENMLNSCHASNPAPQYSWFVNGTFOOSTOELFIPNITVNNSGSYTCQ 300
Db 241 TISPLNTSYRSGENMLNSCHASNPAPQYSWFVNGTFOOSTOELFIPNITVNNSGSYTCQ 300

Qy 241 TISPLNTSYRSGENMLNSCHASNPAPQYSWFVNGTFOOSTOELFIPNITVNNSGSYTCQ 300
Db 241 TISPLNTSYRSGENMLNSCHASNPAPQYSWFVNGTFOOSTOELFIPNITVNNSGSYTCQ 300

Qy 301 AHSNDTGLNRTTYYTITVYAPPKPFTSSNNSNPEVEDDAVALTCEPEIQNTTYLMMVNN 360
Db 301 AHSNDTGLNRTTYYTITVYAPPKPFTSSNNSNPEVEDDAVALTCEPEIQNTTYLMMVNN 360

Qy 301 AHSNDTGLNRTTYYTITVYAPPKPFTSSNNSNPEVEDDAVALTCEPEIQNTTYLMMVNN 360
Db 301 AHSNDTGLNRTTYYTITVYAPPKPFTSSNNSNPEVEDDAVALTCEPEIQNTTYLMMVNN 360

Qy 361 OSLSVSPRLOLSNGNRTTLTSLVTRNDVGPKECGIQNELSDVHSDPVILNLVYGPDDPTI 420
Db 361 OSLSVSPRLOLSNGNRTTLTSLVTRNDVGPKECGIQNELSDVHSDPVILNLVYGPDDPTI 420

Qy 361 OSLSVSPRLOLSNGNRTTLTSLVTRNDVGPKECGIQNELSDVHSDPVILNLVYGPDDPTI 420
Db 361 OSLSVSPRLOLSNGNRTTLTSLVTRNDVGPKECGIQNELSDVHSDPVILNLVYGPDDPTI 420

Qy 421 SPSYTYRPGVNLISLCHASNPAPQYSWMLIDGNIQOHTOELFISNITEKNSGLYTQCAN 480
Db 421 SPSYTYRPGVNLISLCHASNPAPQYSWMLIDGNIQOHTOELFISNITEKNSGLYTQCAN 480

Qy 421 SPSYTYRPGVNLISLCHASNPAPQYSWMLIDGNIQOHTOELFISNITEKNSGLYTQCAN 480
Db 421 SPSYTYRPGVNLISLCHASNPAPQYSWMLIDGNIQOHTOELFISNITEKNSGLYTQCAN 480

Qy 481 NSASGHSRTTAKTIVTSABELPKPSSISNNKPEVEDKDAVAFCEPEAONTTYLMMVNGOS 540
|
Db 481 NSASGHSRTTAKTIVTSABELPKPSSISNNKPEVEDKDAVAFCEPEAONTTYLMMVNGOS 540
Qy 541 LVPSPRLQJNSGNRTTLTENVTRNDARAAYCGIQNSVSANRSDPTLVLYGPDPTIISP 600
|
Db 541 LVPSPRLQJNSGNRTTLTENVTRNDARAAYCGIQNSVSANRSDPTLVLYGPDPTIISP 600
Qy 601 PDSSYLSGANLNLSCHASNPSPQYSWRINGIPQOHTQVLFIAKITPNNNGTYACFVSNTL 660
|
Db 601 PDSSYLSGANLNLSCHASNPSPQYSWRINGIPQOHTQVLFIAKITPNNNGTYACFVSNTL 660
Qy 661 ATGRNNSIVKSIIVTSASGTSFGLSAGATVGMIGLVGVALI 702
|
Db 661 ATGRNNSIVKSIIVTSASGTSFGLSAGATVGMIGLVGVALI 702

RESULT 13
US-10-473-127-1466
; Sequence 1466, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 1466
; LENGTH: 702
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1466

Query Match 100.0%; Score 3721; DB 5; Length 702;
Best Local Similarity 100.0%; Pred. No. 4, 5e-207;
Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MESPSAPPHRMCIIPMORLLTLTASLLTFMNPPTAKLTISTEPNVAEGEVLLVHNLPQ 60
|
Db 1 MESPSAPPHRMCIIPMORLLTLTASLLTFMNPPTAKLTISTEPNVAEGEVLLVHNLPQ 60
Qy 61 HLFGSYWGGERVDGNRQIIGVYIGTQATPGPAYSGREIIYPNASLLIQNIIONDTGXY 120
|
Db 61 HLFGSYWGGERVDGNRQIIGVYIGTQATPGPAYSGREIIYPNASLLIQNIIONDTGXY 120
Qy 121 TLHAVIKSDLVNEEATGQFRVYPELPKPSISSNNKPEVEDKDAVAFCEPEAONTTYLMMV 180
|
Db 121 TLHAVIKSDLVNEEATGQFRVYPELPKPSISSNNKPEVEDKDAVAFCEPEAONTTYLMMV 180
Qy 181 NNOSLPVSPRLQJNSGNRTTLTENVTRNDARAAYCGIQNSVSANRSDPTLVLYGPDPTIISP 240
|
Db 181 NNOSLPVSPRLQJNSGNRTTLTENVTRNDARAAYCGIQNSVSANRSDPTLVLYGPDPTIISP 240
Qy 241 TISPLNTSYRSGENLNLSCHASNPSPQYSWRINGIPQOHTQVLFIAKITPNNNGTYACFVSNTL 300
|
Db 241 TISPLNTSYRSGENLNLSCHASNPSPQYSWRINGIPQOHTQVLFIAKITPNNNGTYACFVSNTL 300
Qy 301 AHNSTGLNRTTITTYVAEPKPEITTSNNSNPEVEDKDAVAFCEPEAONTTYLMMV 360
|
Db 301 AHNSTGLNRTTITTYVAEPKPEITTSNNSNPEVEDKDAVAFCEPEAONTTYLMMV 360

Db 301 AHNSTGLNRTTITTYVAEPKPEITTSNNSNPEVEDKDAVAFCEPEAONTTYLMMV 360
Qy 361 OSLPVSPRLQJNSGNRTTLTENVTRNDARAAYCGIQNSVSANRSDPTLVLYGPDPTIISP 420
|
Db 361 OSLPVSPRLQJNSGNRTTLTENVTRNDARAAYCGIQNSVSANRSDPTLVLYGPDPTIISP 420
Qy 421 SPSSYVYRPGVNLISCHASNPSPQYSWRINGIPQOHTQVLFIAKITPNNNGTYACFVSNTL 480
|
Db 421 SPSSYVYRPGVNLISCHASNPSPQYSWRINGIPQOHTQVLFIAKITPNNNGTYACFVSNTL 480
Qy 481 NSASGHSRTTAKTIVTSABELPKPSSISNNKPEVEDKDAVAFCEPEAONTTYLMMVNGOS 540
|
Db 481 NSASGHSRTTAKTIVTSABELPKPSSISNNKPEVEDKDAVAFCEPEAONTTYLMMVNGOS 540
Qy 541 LVPSPRLQJNSGNRTTLTENVTRNDARAAYCGIQNSVSANRSDPTLVLYGPDPTIISP 600
|
Db 541 LVPSPRLQJNSGNRTTLTENVTRNDARAAYCGIQNSVSANRSDPTLVLYGPDPTIISP 600
Qy 601 PDSSYLSGANLNLSCHASNPSPQYSWRINGIPQOHTQVLFIAKITPNNNGTYACFVSNTL 660
|
Db 601 PDSSYLSGANLNLSCHASNPSPQYSWRINGIPQOHTQVLFIAKITPNNNGTYACFVSNTL 660
Qy 661 ATGRNNSIVKSIIVTSASGTSFGLSAGATVGMIGLVGVALI 702
|
Db 661 ATGRNNSIVKSIIVTSASGTSFGLSAGATVGMIGLVGVALI 702

RESULT 14
US-10-473-127-1500
; Sequence 1500, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 1500
; LENGTH: 702
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1500

Query Match 100.0%; Score 3721; DB 5; Length 702;
Best Local Similarity 100.0%; Pred. No. 4, 5e-207;
Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MESPSAPPHRMCIIPMORLLTLTASLLTFMNPPTAKLTISTEPNVAEGEVLLVHNLPQ 60
|
Db 1 MESPSAPPHRMCIIPMORLLTLTASLLTFMNPPTAKLTISTEPNVAEGEVLLVHNLPQ 60
Qy 61 HLFGSYWGGERVDGNRQIIGVYIGTQATPGPAYSGREIIYPNASLLIQNIIONDTGXY 120
|
Db 61 HLFGSYWGGERVDGNRQIIGVYIGTQATPGPAYSGREIIYPNASLLIQNIIONDTGXY 120
Qy 121 TLHAVIKSDLVNEEATGQFRVYPELPKPSISSNNKPEVEDKDAVAFCEPEAONTTYLMMV 180
|
Db 121 TLHAVIKSDLVNEEATGQFRVYPELPKPSISSNNKPEVEDKDAVAFCEPEAONTTYLMMV 180

```

Qy 181 NNQSLPVSRLQSLNDRRTLLFNTVRNDTASYKETONPVASRRSDSVILANVLYGPDAP 240
Db 181 NNQSLPVSRLQSLNDRRTLLFNTVRNDTASYKETONPVASRRSDSVILANVLYGPDAP 240
Qy 241 TISPLNTSYRSGENILNSCHASANPPOQYSWFVNGTFOOSTOELFIPNITVNNSSGYTCQ 300
Db 241 TISPLNTSYRSGENILNSCHASANPPOQYSWFVNGTFOOSTOELFIPNITVNNSSGYTCQ 300
Qy 301 AHNSTGLNRTVTITTYAEPKPEITSNNSNPVEDDAVALTCPEIONTTYLMMVNN 360
Db 301 AHNSTGLNRTVTITTYAEPKPEITSNNSNPVEDDAVALTCPEIONTTYLMMVNN 360
Qy 361 QSLPVSRLQSLNDRRTLLFNTVRNDVGPYECGIONELSDVHSDPVILANVLYGPDPTI 420
Db 361 QSLPVSRLQSLNDRRTLLFNTVRNDVGPYECGIONELSDVHSDPVILANVLYGPDPTI 420
Qy 421 SPSYTYRPGVNLISCHASANPPOQYSWLIDGNIQOHTOELFISNITEKNSGLYTCQAN 480
Db 421 SPSYTYRPGVNLISCHASANPPOQYSWLIDGNIQOHTOELFISNITEKNSGLYTCQAN 480
Qy 481 NSASGHSRTTYTITVSALPKPSTISSNNSKVEEDKDAVAFCEPAQNTTYLMMVNGOS 540
Db 481 NSASGHSRTTYTITVSALPKPSTISSNNSKVEEDKDAVAFCEPAQNTTYLMMVNGOS 540
Qy 541 LPVSPRLQSLNDRRTLLFNTVRNDARAVYCGIONSVSANRSDPVTLDVLYGPDPTIISP 600
Db 541 LPVSPRLQSLNDRRTLLFNTVRNDARAVYCGIONSVSANRSDPVTLDVLYGPDPTIISP 600
Qy 601 PDSSYLSGANLNLSCHASANPPOQYSWRINGIPQOHTOVLFAKITPPNNGTYACFVSNL 660
Db 601 PDSSYLSGANLNLSCHASANPPOQYSWRINGIPQOHTOVLFAKITPPNNGTYACFVSNL 660
Qy 661 ATGRNNSIVKSTTVASAGTSPGLSAGATVGMIGLVGVALI 702
Db 661 ATGRNNSIVKSTTVASAGTSPGLSAGATVGMIGLVGVALI 702

```

RESULT 15

```

US-10-473-127-1503
; Sequence 1503, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycoo Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1503
; LENGTH: 702
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1503

```

```

Query Match 100.0%; Score 3721; DB 5; Length 702;
Best Local Similarity 100.0%; Pred. No. 4,5e-207;
Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 MESPSAPPHRWCI PMOURLLTASLLTFNNPPTAKLTTESTPFPNVAEGKVLVHNL PQ 60
|||||

```

```

Db 1 MESPSAPPHRWCI PMOURLLTASLLTFNNPPTAKLTTESTPFPNVAEGKVLVHNL PQ 60
Qy 61 HLPFSWYKGERVDGNROIIIGYIGTOQTTPGPAYSGREIIPNABLLIONTI QNDTGFY 120
Db 61 HLPFSWYKGERVDGNROIIIGYIGTOQTTPGPAYSGREIIPNABLLIONTI QNDTGFY 120
Qy 121 TLHVIKSDLVNEEATGQFVPELPKPSISSNNSKVEEDKDAVAFCEPETODATYLMWV 180
Db 121 TLHVIKSDLVNEEATGQFVPELPKPSISSNNSKVEEDKDAVAFCEPETODATYLMWV 180
Qy 181 NNQSLPVSRLQSLNDRRTLLFNTVRNDTASYKETONPVASRRSDSVILANVLYGPDAP 240
Db 181 NNQSLPVSRLQSLNDRRTLLFNTVRNDTASYKETONPVASRRSDSVILANVLYGPDAP 240
Qy 241 TISPLNTSYRSGENILNSCHASANPPOQYSWFVNGTFOOSTOELFIPNITVNNSSGYTCQ 300
Db 241 TISPLNTSYRSGENILNSCHASANPPOQYSWFVNGTFOOSTOELFIPNITVNNSSGYTCQ 300
Qy 301 AHNSTGLNRTVTITTYAEPKPEITSNNSNPVEDDAVALTCPEIONTTYLMMVNN 360
Db 301 AHNSTGLNRTVTITTYAEPKPEITSNNSNPVEDDAVALTCPEIONTTYLMMVNN 360
Qy 361 QSLPVSRLQSLNDRRTLLFNTVRNDVGPYECGIONELSDVHSDPVILANVLYGPDPTI 420
Db 361 QSLPVSRLQSLNDRRTLLFNTVRNDVGPYECGIONELSDVHSDPVILANVLYGPDPTI 420
Qy 421 SPSYTYRPGVNLISCHASANPPOQYSWLIDGNIQOHTOELFISNITEKNSGLYTCQAN 480
Db 421 SPSYTYRPGVNLISCHASANPPOQYSWLIDGNIQOHTOELFISNITEKNSGLYTCQAN 480
Qy 481 NSASGHSRTTYTITVSALPKPSTISSNNSKVEEDKDAVAFCEPAQNTTYLMMVNGOS 540
Db 481 NSASGHSRTTYTITVSALPKPSTISSNNSKVEEDKDAVAFCEPAQNTTYLMMVNGOS 540
Qy 541 LPVSPRLQSLNDRRTLLFNTVRNDARAVYCGIONSVSANRSDPVTLDVLYGPDPTIISP 600
Db 541 LPVSPRLQSLNDRRTLLFNTVRNDARAVYCGIONSVSANRSDPVTLDVLYGPDPTIISP 600
Qy 601 PDSSYLSGANLNLSCHASANPPOQYSWRINGIPQOHTOVLFAKITPPNNGTYACFVSNL 660
Db 601 PDSSYLSGANLNLSCHASANPPOQYSWRINGIPQOHTOVLFAKITPPNNGTYACFVSNL 660
Qy 661 ATGRNNSIVKSTTVASAGTSPGLSAGATVGMIGLVGVALI 702
Db 661 ATGRNNSIVKSTTVASAGTSPGLSAGATVGMIGLVGVALI 702

```

Search completed: April 10, 2006, 18:12:45
 Job time : 181.941 secs

HIS PAGE LEFT BLANK

QY 61 HLFQSWYKGERVDGNRQIIIGVIGTQOATPGPAYSGREIIYPNASLLIQNIIONDTGFY 120
DB 61 HLFQSWYKGERVDGNRQIIIGVIGTQOATPGPAYSGREIIYPNASLLIQNIIONDTGFY 120
QY 121 TLHVKSLVNEBEATGQFRVYBELPKPSISSNNSKPEVDKDAVAFCEPEIQTDAITYLMWV 180
DB 121 TLHVKSLVNEBEATGQFRVYBELPKPSISSNNSKPEVDKDAVAFCEPEIQTDAITYLMWV 180
QY 121 TLHVKSLVNEBEATGQFRVYBELPKPSISSNNSKPEVDKDAVAFCEPEIQTDAITYLMWV 180
DB 121 TLHVKSLVNEBEATGQFRVYBELPKPSISSNNSKPEVDKDAVAFCEPEIQTDAITYLMWV 180
QY 181 NNOSLPVSPRQLOLSNGNRITLTFVNTNRDTSYKCEIQNPVSARSDSVILNVLXGPDAP 240
DB 181 NNOSLPVSPRQLOLSNGNRITLTFVNTNRDTSYKCEIQNPVSARSDSVILNVLXGPDAP 240
QY 241 TISPLNTSYRSGENMLNSCHASNPAPQYSWFVNGTFOQSTQELFIPNITVNNSGSYTCQ 300
DB 241 TISPLNTSYRSGENMLNSCHASNPAPQYSWFVNGTFOQSTQELFIPNITVNNSGSYTCQ 300
QY 301 AHNSDTGLNRTTITVYAEPPKPFITSNNSNPVEDDAVALTCEPEIQNTTYLMMWVN 360
DB 301 AHNSDTGLNRTTITVYAEPPKPFITSNNSNPVEDDAVALTCEPEIQNTTYLMMWVN 360
QY 361 QSLPVSRLQLSNDRITLTLSTVRNDVGPYECIQNELSYDHSDPVILNVLXGPDPTI 420
DB 361 QSLPVSRLQLSNDRITLTLSTVRNDVGPYECIQNELSYDHSDPVILNVLXGPDPTI 420
QY 421 SPSTYTYRPGVNLISLCHAASNPAPQYSWMLIDGNIQOHTQELFISNITEKNSGLYTCQAN 480
DB 421 SPSTYTYRPGVNLISLCHAASNPAPQYSWMLIDGNIQOHTQELFISNITEKNSGLYTCQAN 480
QY 481 NSAGSHRTTYKTTTVAELPKPSISSNNSKPEVDKDAVAFCEPEAQNTTYLMMWVQOS 540
DB 481 NSAGSHRTTYKTTTVAELPKPSISSNNSKPEVDKDAVAFCEPEAQNTTYLMMWVQOS 540
QY 541 LPVSPRQLOLSNGNRITLTFVNTNRDARAYVCGIQNSVANSRSDPTLDVLYGPDPTIISP 600
DB 541 LPVSPRQLOLSNGNRITLTFVNTNRDARAYVCGIQNSVANSRSDPTLDVLYGPDPTIISP 600
QY 601 PDSSYLSGANMLNSCHASNPSPQYSWRINGIPOOHTQVLFIAKITPNNNGTACFVSNL 660
DB 601 PDSSYLSGANMLNSCHASNPSPQYSWRINGIPOOHTQVLFIAKITPNNNGTACFVSNL 660
QY 661 ATGRNNSIVKSIITVASAGTSPGLSAGATVGMIGVLGVALLI 702
DB 661 ATGRNNSIVKSIITVASAGTSPGLSAGATVGMIGVLGVALLI 702

RESULT 4
US-11-051-720-1451
; Sequence 1451, Application US/11051720
; Publication No. US20060046257A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; FILE REFERENCE: 1847.1002
; CURRENT APPLICATION NUMBER: US/11/051.720
; NUMBER OF SEQ ID NOS: 1780
; SEQ ID NO 1451
; LENGTH: 702
; TYPE: PR
; ORGANISM: Homo sapiens
US-11-051-720-1451

Query Match 100.0%; Score 3721; DB 7; Length 702;
Best Local Similarity 100.0%; Pred. No. 1.6e-226;
Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSAPBHRWCIPWOBLLTASLLTFWNPPTAKLTIESPPNVAEGKVLVNLHPQ 60
DB 1 MESSAPBHRWCIPWOBLLTASLLTFWNPPTAKLTIESPPNVAEGKVLVNLHPQ 60
QY 61 HLFQSWYKGERVDGNRQIIIGVIGTQOATPGPAYSGREIIYPNASLLIQNIIONDTGFY 120
DB 61 HLFQSWYKGERVDGNRQIIIGVIGTQOATPGPAYSGREIIYPNASLLIQNIIONDTGFY 120

DB 61 HLFQSWYKGERVDGNRQIIIGVIGTQOATPGPAYSGREIIYPNASLLIQNIIONDTGFY 120
QY 121 TLHVKSLVNEBEATGQFRVYBELPKPSISSNNSKPEVDKDAVAFCEPEIQTDAITYLMWV 180
DB 121 TLHVKSLVNEBEATGQFRVYBELPKPSISSNNSKPEVDKDAVAFCEPEIQTDAITYLMWV 180
QY 121 TLHVKSLVNEBEATGQFRVYBELPKPSISSNNSKPEVDKDAVAFCEPEIQTDAITYLMWV 180
DB 121 TLHVKSLVNEBEATGQFRVYBELPKPSISSNNSKPEVDKDAVAFCEPEIQTDAITYLMWV 180
QY 181 NNOSLPVSPRQLOLSNGNRITLTFVNTNRDTSYKCEIQNPVSARSDSVILNVLXGPDAP 240
DB 181 NNOSLPVSPRQLOLSNGNRITLTFVNTNRDTSYKCEIQNPVSARSDSVILNVLXGPDAP 240
QY 241 TISPLNTSYRSGENMLNSCHASNPAPQYSWFVNGTFOQSTQELFIPNITVNNSGSYTCQ 300
DB 241 TISPLNTSYRSGENMLNSCHASNPAPQYSWFVNGTFOQSTQELFIPNITVNNSGSYTCQ 300
QY 301 AHNSDTGLNRTTITVYAEPPKPFITSNNSNPVEDDAVALTCEPEIQNTTYLMMWVN 360
DB 301 AHNSDTGLNRTTITVYAEPPKPFITSNNSNPVEDDAVALTCEPEIQNTTYLMMWVN 360
QY 361 QSLPVSRLQLSNDRITLTLSTVRNDVGPYECIQNELSYDHSDPVILNVLXGPDPTI 420
DB 361 QSLPVSRLQLSNDRITLTLSTVRNDVGPYECIQNELSYDHSDPVILNVLXGPDPTI 420
QY 421 SPSTYTYRPGVNLISLCHAASNPAPQYSWMLIDGNIQOHTQELFISNITEKNSGLYTCQAN 480
DB 421 SPSTYTYRPGVNLISLCHAASNPAPQYSWMLIDGNIQOHTQELFISNITEKNSGLYTCQAN 480
QY 481 NSAGSHRTTYKTTTVAELPKPSISSNNSKPEVDKDAVAFCEPEAQNTTYLMMWVQOS 540
DB 481 NSAGSHRTTYKTTTVAELPKPSISSNNSKPEVDKDAVAFCEPEAQNTTYLMMWVQOS 540
QY 541 LPVSPRQLOLSNGNRITLTFVNTNRDARAYVCGIQNSVANSRSDPTLDVLYGPDPTIISP 600
DB 541 LPVSPRQLOLSNGNRITLTFVNTNRDARAYVCGIQNSVANSRSDPTLDVLYGPDPTIISP 600
QY 601 PDSSYLSGANMLNSCHASNPSPQYSWRINGIPOOHTQVLFIAKITPNNNGTACFVSNL 660
DB 601 PDSSYLSGANMLNSCHASNPSPQYSWRINGIPOOHTQVLFIAKITPNNNGTACFVSNL 660
QY 661 ATGRNNSIVKSIITVASAGTSPGLSAGATVGMIGVLGVALLI 702
DB 661 ATGRNNSIVKSIITVASAGTSPGLSAGATVGMIGVLGVALLI 702

RESULT 5
US-11-097-252A-2
; Sequence 2, Application US/11097252A
; Publication No. US20060051352A1
; GENERAL INFORMATION:
; APPLICANT: Stemmers, Clifford P.
; APPLICANT: Iliantzis, Christiaan
; TITLE OF INVENTION: Ordoniez-garcia, Cosme
; TITLE OF INVENTION: CEA Binding Agents and Compositions To Reverse CEA-Mediated
; TITLE OF INVENTION: Tumorigenic Effects on Human Cancer Cells, Restore
; FILE REFERENCE: 69029/17
; CURRENT APPLICATION NUMBER: US/11/097.252A
; NUMBER OF SEQ ID NOS: 15
; PRIOR FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: CA2,461,375
; SOFTWARE: Notepad
; SEQ ID NO 2
; LENGTH: 702
; TYPE: PR
; ORGANISM: Homo sapiens
US-11-097-252A-2

Query Match 100.0%; Score 3721; DB 7; Length 702;
Best Local Similarity 100.0%; Pred. No. 1.6e-226;
Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSAPBHRWCIPWOBLLTASLLTFWNPPTAKLTIESPPNVAEGKVLVNLHPQ 60
DB 1 MESSAPBHRWCIPWOBLLTASLLTFWNPPTAKLTIESPPNVAEGKVLVNLHPQ 60
QY 61 HLFQSWYKGERVDGNRQIIIGVIGTQOATPGPAYSGREIIYPNASLLIQNIIONDTGFY 120
DB 61 HLFQSWYKGERVDGNRQIIIGVIGTQOATPGPAYSGREIIYPNASLLIQNIIONDTGFY 120

```
Db      1 MESPAPPHRWCIPMORLLLTASLLTFMNPPTAKLTISTEPFNAEGKEVLLLVHNLQ 60
        61 HLFQSWYGERVDGNROIIIGVIGTQOATPGPAVSGREIYPNASSLIQNIIONDTGY 120
        61 HLFQSWYGERVDGNROIIIGVIGTQOATPGPAVSGREIYPNASSLIQNIIONDTGY 120
Qy      121 TLHAVIKSDLVNEATQGFVRYPELPKPSISSNNSKPEVEDKDAVAFTCEPETODATYLMV 180
        121 TLHAVIKSDLVNEATQGFVRYPELPKPSISSNNSKPEVEDKDAVAFTCEPETODATYLMV 180
Db      121 TLHAVIKSDLVNEATQGFVRYPELPKPSISSNNSKPEVEDKDAVAFTCEPETODATYLMV 180
        121 TLHAVIKSDLVNEATQGFVRYPELPKPSISSNNSKPEVEDKDAVAFTCEPETODATYLMV 180
Qy      181 NNQSLPVSPRLQSLNSGNRTLLTFNVTNRDNTASFKCETONPVASARSDSVIILNLYGPDAP 240
        181 NNQSLPVSPRLQSLNSGNRTLLTFNVTNRDNTASFKCETONPVASARSDSVIILNLYGPDAP 240
Db      181 NNQSLPVSPRLQSLNSGNRTLLTFNVTNRDNTASFKCETONPVASARSDSVIILNLYGPDAP 240
        181 NNQSLPVSPRLQSLNSGNRTLLTFNVTNRDNTASFKCETONPVASARSDSVIILNLYGPDAP 240
Qy      241 TISPLNTSYRSGENLNLSCHAASNPPAOYSWFVNGTFOOSTOELFIPNITVNNSSGYTCQ 300
        241 TISPLNTSYRSGENLNLSCHAASNPPAOYSWFVNGTFOOSTOELFIPNITVNNSSGYTCQ 300
Db      241 TISPLNTSYRSGENLNLSCHAASNPPAOYSWFVNGTFOOSTOELFIPNITVNNSSGYTCQ 300
        241 TISPLNTSYRSGENLNLSCHAASNPPAOYSWFVNGTFOOSTOELFIPNITVNNSSGYTCQ 300
Qy      301 AHNSDTGLNRRTVTTITTYAABPKPEITSNNSNPVEDDAVALTCEPEIQTNTTYLMVNN 360
        301 AHNSDTGLNRRTVTTITTYAABPKPEITSNNSNPVEDDAVALTCEPEIQTNTTYLMVNN 360
Db      301 AHNSDTGLNRRTVTTITTYAABPKPEITSNNSNPVEDDAVALTCEPEIQTNTTYLMVNN 360
        301 AHNSDTGLNRRTVTTITTYAABPKPEITSNNSNPVEDDAVALTCEPEIQTNTTYLMVNN 360
Qy      361 OSIPLVSPRLQSLNSGNRTLLTFNVTNRDNTASFKCETONPVASARSDSVIILNLYGPDAP 420
        361 OSIPLVSPRLQSLNSGNRTLLTFNVTNRDNTASFKCETONPVASARSDSVIILNLYGPDAP 420
Db      361 OSIPLVSPRLQSLNSGNRTLLTFNVTNRDNTASFKCETONPVASARSDSVIILNLYGPDAP 420
        361 OSIPLVSPRLQSLNSGNRTLLTFNVTNRDNTASFKCETONPVASARSDSVIILNLYGPDAP 420
Qy      421 SPSTYTYRPGVNLNLSCHAASNPPAOYSWLDGNIOQHOELFISNTEKNSGLTYCOAN 480
        421 SPSTYTYRPGVNLNLSCHAASNPPAOYSWLDGNIOQHOELFISNTEKNSGLTYCOAN 480
Db      421 SPSTYTYRPGVNLNLSCHAASNPPAOYSWLDGNIOQHOELFISNTEKNSGLTYCOAN 480
        421 SPSTYTYRPGVNLNLSCHAASNPPAOYSWLDGNIOQHOELFISNTEKNSGLTYCOAN 480
Qy      481 NSASGHSRTTVKTTITVSABLPKPSISSNNSKPEVEDKDAVAFTCEPEIQTNTTYLMVNN 540
        481 NSASGHSRTTVKTTITVSABLPKPSISSNNSKPEVEDKDAVAFTCEPEIQTNTTYLMVNN 540
Db      481 NSASGHSRTTVKTTITVSABLPKPSISSNNSKPEVEDKDAVAFTCEPEIQTNTTYLMVNN 540
        481 NSASGHSRTTVKTTITVSABLPKPSISSNNSKPEVEDKDAVAFTCEPEIQTNTTYLMVNN 540
Qy      541 LVPSPRLQSLNSGNRTLLTFNVTNRDNTASFKCETONPVASARSDSVIILNLYGPDAP 600
        541 LVPSPRLQSLNSGNRTLLTFNVTNRDNTASFKCETONPVASARSDSVIILNLYGPDAP 600
Db      541 LVPSPRLQSLNSGNRTLLTFNVTNRDNTASFKCETONPVASARSDSVIILNLYGPDAP 600
        541 LVPSPRLQSLNSGNRTLLTFNVTNRDNTASFKCETONPVASARSDSVIILNLYGPDAP 600
Qy      601 PDSSYSGANLNLSCHASNPSPQYSWRINGIPQOHTOVLFIKTIQPNNGTYACFVSNL 660
        601 PDSSYSGANLNLSCHASNPSPQYSWRINGIPQOHTOVLFIKTIQPNNGTYACFVSNL 660
Db      601 PDSSYSGANLNLSCHASNPSPQYSWRINGIPQOHTOVLFIKTIQPNNGTYACFVSNL 660
        601 PDSSYSGANLNLSCHASNPSPQYSWRINGIPQOHTOVLFIKTIQPNNGTYACFVSNL 660
Qy      661 ATGRNNSIVKSITVSASGTPGLSAGATVGMIGLVGVALI 702
        661 ATGRNNSIVKSITVSASGTPGLSAGATVGMIGLVGVALI 702
Db      661 ATGRNNSIVKSITVSASGTPGLSAGATVGMIGLVGVALI 702
        661 ATGRNNSIVKSITVSASGTPGLSAGATVGMIGLVGVALI 702

RESULT 6
US-10-510-101-68
; Sequence 68, Application US/10510101
; Publication No. US20060018915A1
; GENERAL INFORMATION:
; APPLICANT: Epiimmune Inc.
; APPLICANT: Ishioka, Glenn
; APPLICANT: Fikes, John
; APPLICANT: Tangri, Shabnam
; APPLICANT: Sette, Alessandro
; TITLE OF INVENTION: Heterocyclic Analogs and Related Methods
; FILE REFERENCE: 2060.009PC05
; CURRENT APPLICATION NUMBER: US/10/510.101
; PRIOR FILING DATE: 2004-10-05
; PRIOR APPLICATION NUMBER: US 60/413,471
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 10/116,118
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 68
; LENGTH: 702
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-510-101-68
```

```
Query Match      99.0%; Score 3683; DB 6; Length 702;
Best Local Similarity 99.1%; Pred. No. 4e-224;
Matches 696; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy      1 MESPAPPHRWCIPMORLLLTASLLTFMNPPTAKLTISTEPFNAEGKEVLLLVHNLQ 60
        1 MESPAPPHRWCIPMORLLLTASLLTFMNPPTAKLTISTEPFNAEGKEVLLLVHNLQ 60
Db      1 MESPAPPHRWCIPMORLLLTASLLTFMNPPTAKLTISTEPFNAEGKEVLLLVHNLQ 60
        1 MESPAPPHRWCIPMORLLLTASLLTFMNPPTAKLTISTEPFNAEGKEVLLLVHNLQ 60
Qy      61 HLFQSWYGERVDGNROIIIGVIGTQOATPGPAVSGREIYPNASSLIQNIIONDTGY 120
        61 HLFQSWYGERVDGNROIIIGVIGTQOATPGPAVSGREIYPNASSLIQNIIONDTGY 120
Db      61 HLFQSWYGERVDGNROIIIGVIGTQOATPGPAVSGREIYPNASSLIQNIIONDTGY 120
        61 HLFQSWYGERVDGNROIIIGVIGTQOATPGPAVSGREIYPNASSLIQNIIONDTGY 120
Qy      121 TLHAVIKSDLVNEATQGFVRYPELPKPSISSNNSKPEVEDKDAVAFTCEPETODATYLMV 180
        121 TLHAVIKSDLVNEATQGFVRYPELPKPSISSNNSKPEVEDKDAVAFTCEPETODATYLMV 180
Db      121 TLHAVIKSDLVNEATQGFVRYPELPKPSISSNNSKPEVEDKDAVAFTCEPETODATYLMV 180
        121 TLHAVIKSDLVNEATQGFVRYPELPKPSISSNNSKPEVEDKDAVAFTCEPETODATYLMV 180
Qy      181 NNQSLPVSPRLQSLNSGNRTLLTFNVTNRDNTASFKCETONPVASARSDSVIILNLYGPDAP 240
        181 NNQSLPVSPRLQSLNSGNRTLLTFNVTNRDNTASFKCETONPVASARSDSVIILNLYGPDAP 240
Db      181 NNQSLPVSPRLQSLNSGNRTLLTFNVTNRDNTASFKCETONPVASARSDSVIILNLYGPDAP 240
        181 NNQSLPVSPRLQSLNSGNRTLLTFNVTNRDNTASFKCETONPVASARSDSVIILNLYGPDAP 240
Qy      241 TISPLNTSYRSGENLNLSCHAASNPPAOYSWFVNGTFOOSTOELFIPNITVNNSSGYTCQ 300
        241 TISPLNTSYRSGENLNLSCHAASNPPAOYSWFVNGTFOOSTOELFIPNITVNNSSGYTCQ 300
Db      241 TISPLNTSYRSGENLNLSCHAASNPPAOYSWFVNGTFOOSTOELFIPNITVNNSSGYTCQ 300
        241 TISPLNTSYRSGENLNLSCHAASNPPAOYSWFVNGTFOOSTOELFIPNITVNNSSGYTCQ 300
Qy      301 AHNSDTGLNRRTVTTITTYAABPKPEITSNNSNPVEDDAVALTCEPEIQTNTTYLMVNN 360
        301 AHNSDTGLNRRTVTTITTYAABPKPEITSNNSNPVEDDAVALTCEPEIQTNTTYLMVNN 360
Db      301 AHNSDTGLNRRTVTTITTYAABPKPEITSNNSNPVEDDAVALTCEPEIQTNTTYLMVNN 360
        301 AHNSDTGLNRRTVTTITTYAABPKPEITSNNSNPVEDDAVALTCEPEIQTNTTYLMVNN 360
Qy      361 OSIPLVSPRLQSLNSGNRTLLTFNVTNRDNTASFKCETONPVASARSDSVIILNLYGPDAP 420
        361 OSIPLVSPRLQSLNSGNRTLLTFNVTNRDNTASFKCETONPVASARSDSVIILNLYGPDAP 420
Db      361 OSIPLVSPRLQSLNSGNRTLLTFNVTNRDNTASFKCETONPVASARSDSVIILNLYGPDAP 420
        361 OSIPLVSPRLQSLNSGNRTLLTFNVTNRDNTASFKCETONPVASARSDSVIILNLYGPDAP 420
Qy      421 SPSTYTYRPGVNLNLSCHAASNPPAOYSWLDGNIOQHOELFISNTEKNSGLTYCOAN 480
        421 SPSTYTYRPGVNLNLSCHAASNPPAOYSWLDGNIOQHOELFISNTEKNSGLTYCOAN 480
Db      421 SPSTYTYRPGVNLNLSCHAASNPPAOYSWLDGNIOQHOELFISNTEKNSGLTYCOAN 480
        421 SPSTYTYRPGVNLNLSCHAASNPPAOYSWLDGNIOQHOELFISNTEKNSGLTYCOAN 480
Qy      481 NSASGHSRTTVKTTITVSABLPKPSISSNNSKPEVEDKDAVAFTCEPEIQTNTTYLMVNN 540
        481 NSASGHSRTTVKTTITVSABLPKPSISSNNSKPEVEDKDAVAFTCEPEIQTNTTYLMVNN 540
Db      481 NSASGHSRTTVKTTITVSABLPKPSISSNNSKPEVEDKDAVAFTCEPEIQTNTTYLMVNN 540
        481 NSASGHSRTTVKTTITVSABLPKPSISSNNSKPEVEDKDAVAFTCEPEIQTNTTYLMVNN 540
Qy      541 LVPSPRLQSLNSGNRTLLTFNVTNRDNTASFKCETONPVASARSDSVIILNLYGPDAP 600
        541 LVPSPRLQSLNSGNRTLLTFNVTNRDNTASFKCETONPVASARSDSVIILNLYGPDAP 600
Db      541 LVPSPRLQSLNSGNRTLLTFNVTNRDNTASFKCETONPVASARSDSVIILNLYGPDAP 600
        541 LVPSPRLQSLNSGNRTLLTFNVTNRDNTASFKCETONPVASARSDSVIILNLYGPDAP 600
Qy      601 PDSSYSGANLNLSCHASNPSPQYSWRINGIPQOHTOVLFIKTIQPNNGTYACFVSNL 660
        601 PDSSYSGANLNLSCHASNPSPQYSWRINGIPQOHTOVLFIKTIQPNNGTYACFVSNL 660
Db      601 PDSSYSGANLNLSCHASNPSPQYSWRINGIPQOHTOVLFIKTIQPNNGTYACFVSNL 660
        601 PDSSYSGANLNLSCHASNPSPQYSWRINGIPQOHTOVLFIKTIQPNNGTYACFVSNL 660
Qy      661 ATGRNNSIVKSITVSASGTPGLSAGATVGMIGLVGVALI 702
        661 ATGRNNSIVKSITVSASGTPGLSAGATVGMIGLVGVALI 702
Db      661 ATGRNNSIVKSITVSASGTPGLSAGATVGMIGLVGVALI 702
        661 ATGRNNSIVKSITVSASGTPGLSAGATVGMIGLVGVALI 702

RESULT 7
US-11-050-857-551
; Sequence 551, Application US/11050857
; Publication No. US20060040278A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; FILE REFERENCE: 1847.1005
; CURRENT APPLICATION NUMBER: US/11/050,857
; PRIOR FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1150
; SEQ ID NO 551
; LENGTH: 719
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-050-857-551
```

Query Match 96.8%; Score 3601.5; DB 7; Length 719;
Best Local Similarity 99.1%; Pred. No. 5.4e-219;

Matches 679; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

```
OY 1 MESPSAPPHRMCIPMORLLLTASLLTFMNPPTAKLTISTEPNVAEGEVLLVHNLPO 60
DB 1 MESPSAPPHRMCIPMORLLLTASLLTFMNPPTAKLTISTEPNVAEGEVLLVHNLPO 60
OY 61 HLFQSWYKGERVDGNROIIIGVIGTQOATPGPAYSGREIIYPNASLLIIONIIQNDGFR 120
DB 61 HLFQSWYKGERVDGNROIIIGVIGTQOATPGPAYSGREIIYPNASLLIIONIIQNDGFR 120
OY 121 TLHAVIKSDLVNEEATGQFRVYPELPKPSISSNNSKVEDKDAVAFTCEPETODATYLMWV 180
DB 121 TLHAVIKSDLVNEEATGQFRVYPELPKPSISSNNSKVEDKDAVAFTCEPETODATYLMWV 180
OY 121 TLHAVIKSDLVNEEATGQFRVYPELPKPSISSNNSKVEDKDAVAFTCEPETODATYLMWV 180
DB 121 TLHAVIKSDLVNEEATGQFRVYPELPKPSISSNNSKVEDKDAVAFTCEPETODATYLMWV 180
OY 161 NNQSLPVSRLQSLNSGNRTLTFNTRNDTASYKETONPVARSDSVILVNLGPDAP 240
DB 161 NNQSLPVSRLQSLNSGNRTLTFNTRNDTASYKETONPVARSDSVILVNLGPDAP 240
OY 241 TISPLNTSYRSGENLNSCHASNPAPQYSWFVNGTFOOSTOELFIPNITVNNSSGYTCQ 300
DB 241 TISPLNTSYRSGENLNSCHASNPAPQYSWFVNGTFOOSTOELFIPNITVNNSSGYTCQ 300
OY 301 AHNSTGLNRTTITVYAEPPKPFITSNNSNPVEDDAVALTCEPEIQTNTTYLMWVNN 360
DB 301 AHNSTGLNRTTITVYAEPPKPFITSNNSNPVEDDAVALTCEPEIQTNTTYLMWVNN 360
OY 361 OSLPVSRLQSLNSGNRTLTLSTVTRNDVGPYECGIONELSDHSDPVILNVLGPDPTI 420
DB 361 OSLPVSRLQSLNSGNRTLTLSTVTRNDVGPYECGIONELSDHSDPVILNVLGPDPTI 420
OY 421 SPSTYTRPGVNLISCHASNPAPQYSWMLIDGNIQOHTOELFISNTEKNSGLYTCCAN 480
DB 421 SPSTYTRPGVNLISCHASNPAPQYSWMLIDGNIQOHTOELFISNTEKNSGLYTCCAN 480
OY 481 NSAGSHRTTYKTTIVSAELPKPSISSNNSKVEDKDAVAFTCEPEIQTNTTYLMWVNN 540
DB 481 NSAGSHRTTYKTTIVSAELPKPSISSNNSKVEDKDAVAFTCEPEIQTNTTYLMWVNN 540
OY 541 LPVSPRLQSLNSGNRTLTFNTRNDARAYVCGIONSVANSNDPVTLDVLYGPDPTIIS 600
DB 541 LPVSPRLQSLNSGNRTLTFNTRNDARAYVCGIONSVANSNDPVTLDVLYGPDPTIIS 600
OY 601 PDSSYLSGANLNLCHSASNPSPQYSWRINGIPOOHTOVLFIKITTNNNGTYACFVSNL 660
DB 601 PDSSYLSGANLNLCHSASNPSPQYSWRINGIPOOHTOVLFIKITTNNNGTYACFVSNL 660
OY 661 ATGRNNSIVKSIIVSASGTSPLSA 685
DB 661 ATGRNNSIVKSIIVSASGTSPLSA 685
```

RESULT 8

US-11-051-720-1381
; Sequence 1381, Application US/11051720
; Publication No. US20060046257A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; FILE REFERENCE: 1847.1002
; CURRENT APPLICATION NUMBER: US/11/051.720
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1780
; SEQ ID NO 1381
; LENGTH: 719
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-051-720-1381

Query Match 96.8%; Score 3601.5; DB 7; Length 719;
Best Local Similarity 99.1%; Pred. No. 5.4e-219;
Matches 679; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

```
OY 1 MESPSAPPHRMCIPMORLLLTASLLTFMNPPTAKLTISTEPNVAEGEVLLVHNLPO 60
DB 1 MESPSAPPHRMCIPMORLLLTASLLTFMNPPTAKLTISTEPNVAEGEVLLVHNLPO 60
OY 61 HLFQSWYKGERVDGNROIIIGVIGTQOATPGPAYSGREIIYPNASLLIIONIIQNDGFR 120
DB 61 HLFQSWYKGERVDGNROIIIGVIGTQOATPGPAYSGREIIYPNASLLIIONIIQNDGFR 120
OY 121 TLHAVIKSDLVNEEATGQFRVYPELPKPSISSNNSKVEDKDAVAFTCEPETODATYLMWV 180
DB 121 TLHAVIKSDLVNEEATGQFRVYPELPKPSISSNNSKVEDKDAVAFTCEPETODATYLMWV 180
OY 121 TLHAVIKSDLVNEEATGQFRVYPELPKPSISSNNSKVEDKDAVAFTCEPETODATYLMWV 180
DB 121 TLHAVIKSDLVNEEATGQFRVYPELPKPSISSNNSKVEDKDAVAFTCEPETODATYLMWV 180
OY 161 NNQSLPVSRLQSLNSGNRTLTFNTRNDTASYKETONPVARSDSVILVNLGPDAP 240
DB 161 NNQSLPVSRLQSLNSGNRTLTFNTRNDTASYKETONPVARSDSVILVNLGPDAP 240
OY 241 TISPLNTSYRSGENLNSCHASNPAPQYSWFVNGTFOOSTOELFIPNITVNNSSGYTCQ 300
DB 241 TISPLNTSYRSGENLNSCHASNPAPQYSWFVNGTFOOSTOELFIPNITVNNSSGYTCQ 300
OY 301 AHNSTGLNRTTITVYAEPPKPFITSNNSNPVEDDAVALTCEPEIQTNTTYLMWVNN 360
DB 301 AHNSTGLNRTTITVYAEPPKPFITSNNSNPVEDDAVALTCEPEIQTNTTYLMWVNN 360
OY 361 OSLPVSRLQSLNSGNRTLTLSTVTRNDVGPYECGIONELSDHSDPVILNVLGPDPTI 420
DB 361 OSLPVSRLQSLNSGNRTLTLSTVTRNDVGPYECGIONELSDHSDPVILNVLGPDPTI 420
OY 421 SPSTYTRPGVNLISCHASNPAPQYSWMLIDGNIQOHTOELFISNTEKNSGLYTCCAN 480
DB 421 SPSTYTRPGVNLISCHASNPAPQYSWMLIDGNIQOHTOELFISNTEKNSGLYTCCAN 480
OY 481 NSAGSHRTTYKTTIVSAELPKPSISSNNSKVEDKDAVAFTCEPEIQTNTTYLMWVNN 540
DB 481 NSAGSHRTTYKTTIVSAELPKPSISSNNSKVEDKDAVAFTCEPEIQTNTTYLMWVNN 540
OY 541 LPVSPRLQSLNSGNRTLTFNTRNDARAYVCGIONSVANSNDPVTLDVLYGPDPTIIS 600
DB 541 LPVSPRLQSLNSGNRTLTFNTRNDARAYVCGIONSVANSNDPVTLDVLYGPDPTIIS 600
OY 601 PDSSYLSGANLNLCHSASNPSPQYSWRINGIPOOHTOVLFIKITTNNNGTYACFVSNL 660
DB 601 PDSSYLSGANLNLCHSASNPSPQYSWRINGIPOOHTOVLFIKITTNNNGTYACFVSNL 660
OY 661 ATGRNNSIVKSIIVSASGTSPLSA 685
DB 661 ATGRNNSIVKSIIVSASGTSPLSA 685
```

RESULT 9

US-11-050-857-552
; Sequence 552, Application US/11050857
; Publication No. US20060040278A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; FILE REFERENCE: 1847.1005
; CURRENT APPLICATION NUMBER: US/11/050.857
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1150
; SEQ ID NO 552
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-050-857-552

Query Match 79.8%; Score 2968; DB 7; Length 569;
Best Local Similarity 98.1%; Pred. No. 2.7e-179;
Matches 556; Conservative 2; Mismatches 9; Indels 0; Gaps 0;
OY 1 MESPSAPPHRMCIPMORLLLTASLLTFMNPPTAKLTISTEPNVAEGEVLLVHNLPO 60

Db 1 MESPSAPPHRWCI PMORLLTASLLTFMNPPTAKLTIESSTEPNVAEGKEVLLVHNLPO 60
Qy 61 HLFQSWYGERVDGNRQIIIGVIGTQATPGPAYSGREIYPNASLLIIONTIQNDTGFY 120
Db 61 HLFQSWYGERVDGNRQIIIGVIGTQATPGPAYSGREIYPNASLLIIONTIQNDTGFY 120
Qy 121 TLHVKSIDLVBNEATQGFYRYPPEL PKPSISSNNSKPEVDKDAVAFTCEPETQATYLMWV 180
Db 121 TLHVKSIDLVBNEATQGFYRYPPEL PKPSISSNNSKPEVDKDAVAFTCEPETQATYLMWV 180
Qy 181 NNQSLPVSRLQSLNSGNRTLLTFNVRNDTAS YKCETONPVSARRSDSVILNLVYGPDPAP 240
Db 181 NNQSLPVSRLQSLNSGNRTLLTFNVRNDTAS YKCETONPVSARRSDSVILNLVYGPDPAP 240
Qy 241 TISPLNTSYRSGENLNLSCHAA SNPQAQSWFNGTFOOSTOELFIPNITVNNSSGYTCQ 300
Db 241 TISPLNTSYRSGENLNLSCHAA SNPQAQSWFNGTFOOSTOELFIPNITVNNSSGYTCQ 300
Qy 301 AHNSDTGLNRTVTYTTIYVAEPKPFITSNNSNPVEDDAVALTCEPEIQTNTTYLMWVN 360
Db 301 AHNSDTGLNRTVTYTTIYVAEPKPFITSNNSNPVEDDAVALTCEPEIQTNTTYLMWVN 360
Qy 361 OSIPLVSPRLQSLNSGNRTLLTFNVRNDTAS YKCETONPVSARRSDSVILNLVYGPDPAP 420
Db 361 OSIPLVSPRLQSLNSGNRTLLTFNVRNDTAS YKCETONPVSARRSDSVILNLVYGPDPAP 420
Qy 421 SPSTYTYRPGVNLISCHAA SNPQAQSWFNGTFOOSTOELFIPNITVNNSSGYTCQ 480
Db 421 SPSTYTYRPGVNLISCHAA SNPQAQSWFNGTFOOSTOELFIPNITVNNSSGYTCQ 480
Qy 481 NSASGHSRTTVKTIYVSAELPKPSISSNNSKPEVDKDAVAFTCEPEIQTNTTYLMWVN 540
Db 481 NSASGHSRTTVKTIYVSAELPKPSISSNNSKPEVDKDAVAFTCEPEIQTNTTYLMWVN 540
Qy 541 LPVSPRLQSLNSGNRTLLTFNVRNDTAS YKCETONPVSARRSDSVILNLVYGPDPAP 567
Db 541 LPVSPRLQSLNSGNRTLLTFNVRNDTAS YKCETONPVSARRSDSVILNLVYGPDPAP 567

RESULT 10
US-11-051-720-1382
; Sequence 1382, Application US/11051720
; Publication No. US20060046257A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 1847.1002
; CURRENT APPLICATION NUMBER: US/11/051.720
; NUMBER OF SEQ ID NOS: 1780
; SEQ ID NO 1382
; LENGTH: 569
; TYPE: PRN
; ORGANISM: Homo sapiens
US-11-051-720-1382

Query Match 79.8%; Score 2968; DB 7; Length 569;
Best Local Similarity 98.1%; Pred. No. 2.7e-179;
Matches 556; Conservative 2; Mismatches 9; Indels 0; Gaps 0;
Qy 1 MESPSAPPHRWCI PMORLLTASLLTFMNPPTAKLTIESSTEPNVAEGKEVLLVHNLPO 60
Db 1 MESPSAPPHRWCI PMORLLTASLLTFMNPPTAKLTIESSTEPNVAEGKEVLLVHNLPO 60
Qy 61 HLFQSWYGERVDGNRQIIIGVIGTQATPGPAYSGREIYPNASLLIIONTIQNDTGFY 120
Db 61 HLFQSWYGERVDGNRQIIIGVIGTQATPGPAYSGREIYPNASLLIIONTIQNDTGFY 120
Qy 121 TLHVKSIDLVBNEATQGFYRYPPEL PKPSISSNNSKPEVDKDAVAFTCEPETQATYLMWV 180
Db 121 TLHVKSIDLVBNEATQGFYRYPPEL PKPSISSNNSKPEVDKDAVAFTCEPETQATYLMWV 180

Qy 181 NNQSLPVSRLQSLNSGNRTLLTFNVRNDTAS YKCETONPVSARRSDSVILNLVYGPDPAP 240
Db 181 NNQSLPVSRLQSLNSGNRTLLTFNVRNDTAS YKCETONPVSARRSDSVILNLVYGPDPAP 240
Qy 241 TISPLNTSYRSGENLNLSCHAA SNPQAQSWFNGTFOOSTOELFIPNITVNNSSGYTCQ 300
Db 241 TISPLNTSYRSGENLNLSCHAA SNPQAQSWFNGTFOOSTOELFIPNITVNNSSGYTCQ 300
Qy 301 AHNSDTGLNRTVTYTTIYVAEPKPFITSNNSNPVEDDAVALTCEPEIQTNTTYLMWVN 360
Db 301 AHNSDTGLNRTVTYTTIYVAEPKPFITSNNSNPVEDDAVALTCEPEIQTNTTYLMWVN 360
Qy 361 OSIPLVSPRLQSLNSGNRTLLTFNVRNDTAS YKCETONPVSARRSDSVILNLVYGPDPAP 420
Db 361 OSIPLVSPRLQSLNSGNRTLLTFNVRNDTAS YKCETONPVSARRSDSVILNLVYGPDPAP 420
Qy 421 SPSTYTYRPGVNLISCHAA SNPQAQSWFNGTFOOSTOELFIPNITVNNSSGYTCQ 480
Db 421 SPSTYTYRPGVNLISCHAA SNPQAQSWFNGTFOOSTOELFIPNITVNNSSGYTCQ 480
Qy 481 NSASGHSRTTVKTIYVSAELPKPSISSNNSKPEVDKDAVAFTCEPEIQTNTTYLMWVN 540
Db 481 NSASGHSRTTVKTIYVSAELPKPSISSNNSKPEVDKDAVAFTCEPEIQTNTTYLMWVN 540
Qy 541 LPVSPRLQSLNSGNRTLLTFNVRNDTAS YKCETONPVSARRSDSVILNLVYGPDPAP 567
Db 541 LPVSPRLQSLNSGNRTLLTFNVRNDTAS YKCETONPVSARRSDSVILNLVYGPDPAP 567

RESULT 11
US-11-050-857-554
; Sequence 554, Application US/11050857
; Publication No. US20060040278A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 1847.1005
; CURRENT APPLICATION NUMBER: US/11/050.857
; NUMBER OF SEQ ID NOS: 1150
; SEQ ID NO 554
; LENGTH: 346
; TYPE: PRN
; ORGANISM: Homo sapiens
US-11-050-857-554

Query Match 44.0%; Score 1637; DB 7; Length 346;
Best Local Similarity 49.3%; Pred. No. 6.5e-96;
Matches 346; Conservative 0; Mismatches 0; Indels 356; Gaps 1;
Qy 1 MESPSAPPHRWCI PMORLLTASLLTFMNPPTAKLTIESSTEPNVAEGKEVLLVHNLPO 60
Db 1 MESPSAPPHRWCI PMORLLTASLLTFMNPPTAKLTIESSTEPNVAEGKEVLLVHNLPO 60
Qy 61 HLFQSWYGERVDGNRQIIIGVIGTQATPGPAYSGREIYPNASLLIIONTIQNDTGFY 120
Db 61 HLFQSWYGERVDGNRQIIIGVIGTQATPGPAYSGREIYPNASLLIIONTIQNDTGFY 120
Qy 121 TLHVKSIDLVBNEATQGFYRYPPEL PKPSISSNNSKPEVDKDAVAFTCEPETQATYLMWV 180
Db 121 TLHVKSIDLVBNEATQGFYRYPPEL PKPSISSNNSKPEVDKDAVAFTCEPETQATYLMWV 180
Qy 143 ----- 142
Db 241 TISPLNTSYRSGENLNLSCHAA SNPQAQSWFNGTFOOSTOELFIPNITVNNSSGYTCQ 300
Qy 143 ----- 142
Db 301 AHNSDTGLNRTVTYTTIYVAEPKPFITSNNSNPVEDDAVALTCEPEIQTNTTYLMWVN 360

Db 143 ----- 142
Qy 361 QSLPVSRLQSLNDNRKTLTLLSVTRNDVGPYECGIONELSYDSDPVLINLVYGPDDPTI 420
Db 143 ----- 142
Qy 421 SPSTYTYRPGVNLISLCHAASNPAPQYSWLDIGNIQHTQELFISNTEKNSGLTYCOAN 480
Db 143 ----- 142
Qy 481 NSAGSHRTYKTTIVSAELPKPSSISNNSKPEVDKDAVAFCEBEAQNTTYLMMVNGQS 540
Db 143 ----- ELPKPSSISNNSKPEVDKDAVAFCEBEAQNTTYLMMVNGQS 184
Qy 541 LPVSPRLQSLNGNRRLTLFNTVRNDARAYVCGIQNSVANSRSDPVTLDVLVYGPDPPIISP 600
Db 185 LPVSPRLQSLNGNRRLTLFNTVRNDARAYVCGIQNSVANSRSDPVTLDVLVYGPDPPIISP 244
Qy 601 PDSSTLSGANLNLSCHSASNPSPQYSWRINGIPOOHTQVLFIAKITPPNNNGTYACFVSNL 660
Db 245 PDSSTLSGANLNLSCHSASNPSPQYSWRINGIPOOHTQVLFIAKITPPNNNGTYACFVSNL 304
Qy 661 ATGRNNSIVKSIIVSASGTSFGLSAGATVGMIGLVGVALLI 702
Db 305 ATGRNNSIVKSIIVSASGTSFGLSAGATVGMIGLVGVALLI 346

RESULT 12
US-11-051-720-1384
; Sequence 1384, Application US/11051720
; Publication No. US20060046257A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 1847.1002
; CURRENT APPLICATION NUMBER: US/11/051,720
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1780
; SEQ ID NO 1384
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-051-720-1384

Query Match 44.0%; Score 1637; DB 7; Length 346;
Best Local Similarity 49.3%; Pred. No. 6.5e-96;
Matches 346; Conservative 0; Mismatches 0; Indels 356; Gaps 1;

Qy 1 MESPSAPHRWCIPWQRLTLFASLLTFMNPPTAKLTTESTPPNVAEGEVLLVHNLPO 60
Db 1 MESPSAPHRWCIPWQRLTLFASLLTFMNPPTAKLTTESTPPNVAEGEVLLVHNLPO 60
Qy 61 HLFQSWYKGRVDGNRQIIGYVIGTQOATPGPAYSGREIITYPNASLLIONIONDTGFY 120
Db 61 HLFQSWYKGRVDGNRQIIGYVIGTQOATPGPAYSGREIITYPNASLLIONIONDTGFY 120
Qy 121 TLHVIKSDLVNEAATGQFRVYPELPKPSISSNNSKPEVDKDAVAFCEBEAQNTTYLMMV 180
Db 121 TLHVIKSDLVNEAATGQFRVYPELPKPSISSNNSKPEVDKDAVAFCEBEAQNTTYLMMV 180
Qy 181 NNQSLPVSRLQSLNGNRRLTLFNTVRNDARAYVCGIQNSVANSRSDPVTLDVLVYGPDP 240
Db 181 NNQSLPVSRLQSLNGNRRLTLFNTVRNDARAYVCGIQNSVANSRSDPVTLDVLVYGPDP 240
Qy 241 TISPLNTSYSGENLNLSCHAASNPAPQYSWLVNGTFOQSTQELFIPNITVNNSGSYTCQ 300
Db 241 TISPLNTSYSGENLNLSCHAASNPAPQYSWLVNGTFOQSTQELFIPNITVNNSGSYTCQ 300
Qy 301 AHNSDTGLNRTTTLITVYAEPPKPFITSNNSNPEVEDADAVALTCEPEIQNTTYLMMVNN 360
Db 301 AHNSDTGLNRTTTLITVYAEPPKPFITSNNSNPEVEDADAVALTCEPEIQNTTYLMMVNN 360
Qy 143 ----- 142
Qy 143 ----- 142

Qy 361 QSLPVSRLQSLNDNRKTLTLLSVTRNDVGPYECGIONELSYDSDPVLINLVYGPDDPTI 420
Db 143 ----- 142
Qy 421 SPSTYTYRPGVNLISLCHAASNPAPQYSWLDIGNIQHTQELFISNTEKNSGLTYCOAN 480
Db 143 ----- 142
Qy 481 NSAGSHRTYKTTIVSAELPKPSSISNNSKPEVDKDAVAFCEBEAQNTTYLMMVNGQS 540
Db 143 ----- ELPKPSSISNNSKPEVDKDAVAFCEBEAQNTTYLMMVNGQS 184
Qy 541 LPVSPRLQSLNGNRRLTLFNTVRNDARAYVCGIQNSVANSRSDPVTLDVLVYGPDPPIISP 600
Db 185 LPVSPRLQSLNGNRRLTLFNTVRNDARAYVCGIQNSVANSRSDPVTLDVLVYGPDPPIISP 244
Qy 601 PDSSTLSGANLNLSCHSASNPSPQYSWRINGIPOOHTQVLFIAKITPPNNNGTYACFVSNL 660
Db 245 PDSSTLSGANLNLSCHSASNPSPQYSWRINGIPOOHTQVLFIAKITPPNNNGTYACFVSNL 304
Qy 661 ATGRNNSIVKSIIVSASGTSFGLSAGATVGMIGLVGVALLI 702
Db 305 ATGRNNSIVKSIIVSASGTSFGLSAGATVGMIGLVGVALLI 346

RESULT 13
US-11-050-857-553
; Sequence 553, Application US/11050857
; Publication No. US20060040278A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 1847.1005
; CURRENT APPLICATION NUMBER: US/11/050,857
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1150
; SEQ ID NO 553
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-050-857-553

Query Match 44.0%; Score 1636; DB 7; Length 346;
Best Local Similarity 49.3%; Pred. No. 7.5e-96;
Matches 346; Conservative 0; Mismatches 0; Indels 356; Gaps 1;

Qy 1 MESPSAPHRWCIPWQRLTLFASLLTFMNPPTAKLTTESTPPNVAEGEVLLVHNLPO 60
Db 1 MESPSAPHRWCIPWQRLTLFASLLTFMNPPTAKLTTESTPPNVAEGEVLLVHNLPO 60
Qy 61 HLFQSWYKGRVDGNRQIIGYVIGTQOATPGPAYSGREIITYPNASLLIONIONDTGFY 120
Db 61 HLFQSWYKGRVDGNRQIIGYVIGTQOATPGPAYSGREIITYPNASLLIONIONDTGFY 120
Qy 121 TLHVIKSDLVNEAATGQFRVYPELPKPSISSNNSKPEVDKDAVAFCEBEAQNTTYLMMV 180
Db 121 TLHVIKSDLVNEAATGQFRVYPELPKPSISSNNSKPEVDKDAVAFCEBEAQNTTYLMMV 180
Qy 181 NNQSLPVSRLQSLNGNRRLTLFNTVRNDARAYVCGIQNSVANSRSDPVTLDVLVYGPDP 240
Db 181 NNQSLPVSRLQSLNGNRRLTLFNTVRNDARAYVCGIQNSVANSRSDPVTLDVLVYGPDP 240
Qy 241 TISPLNTSYSGENLNLSCHAASNPAPQYSWLVNGTFOQSTQELFIPNITVNNSGSYTCQ 300
Db 241 TISPLNTSYSGENLNLSCHAASNPAPQYSWLVNGTFOQSTQELFIPNITVNNSGSYTCQ 300
Qy 301 AHNSDTGLNRTTTLITVYAEPPKPFITSNNSNPEVEDADAVALTCEPEIQNTTYLMMVNN 360
Db 301 AHNSDTGLNRTTTLITVYAEPPKPFITSNNSNPEVEDADAVALTCEPEIQNTTYLMMVNN 360
Qy 361 QSLPVSRLQSLNDNRKTLTLLSVTRNDVGPYECGIONELSYDSDPVLINLVYGPDDPTI 420

Db 233 ----- 232
QY 421 SPSYTYRPGVNLISLSCHAASNPAPQYSMLIDGNIQHTOELFISNTEKNSGLTYCOAN 480
Db 233 ----- 232
QY 481 NSAGSHSRTTYKTTIVSAELPKPSISSNNSKPEVDKAVAFCEPEAONTTYLMMVNGOS 540
Db 233 ----- 232
QY 541 LPVSPRLQLSNGNRTLTLFNVTRNDARAVYCGIQNSVANSRSDPVTLDVLYGPDPTIISP 600
Db 233 ----- 244
QY 601 PDSSYLSGANLNLSCSHASNPSPQYSWRINGIPQOHTOVLFLAKITPNNNGTYACFVSNL 660
Db 245 PDSSYLSGANLNLSCSHASNPSPQYSWRINGIPQOHTOVLFLAKITPNNNGTYACFVSNL 304
QY 661 ATGRNNSIVKSIIVTSASGTSPLSAGATVGMIGVLGVVALI 702
Db 305 ATGRNNSIVKSIIVTSASGTSPLSAGATVGMIGVLGVVALI 346

RESULT 14
US-11-051-720-1383
; Sequence 1383, Application US/11051720
; Publication No. US20060046257A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; FILE REFERENCE: 1847.1002
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1780
; SEQ ID NO 1383
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-051-720-1383

Query Match 44.0%; Score 1636; DB 7; Length 346;
Best Local Similarity 49.3%; Pred. No. 7.5e-96;
Matches 346; Conservative 0; Mismatches 0; Indels 356; Gaps 1;
QY 1 MESPSAPPHRMCTPMQRLTLTASLTFMNPPTAKLTITESTPPNVAEGKEVLLVHNLPQ 60
Db 1 MESPSAPPHRMCTPMQRLTLTASLTFMNPPTAKLTITESTPPNVAEGKEVLLVHNLPQ 60
QY 61 HLFYGMVYGERVDGNROITIGVIGTQOATPGPAYSGREIITYPNASLLIIONITQNDTGFY 120
Db 61 HLFYGMVYGERVDGNROITIGVIGTQOATPGPAYSGREIITYPNASLLIIONITQNDTGFY 120
QY 121 TLHVIKSDLVNEBAGTQFRVYPELPKPSISSNNSKPEVDKAVAFCEPEAONTTYLMMV 180
Db 121 TLHVIKSDLVNEBAGTQFRVYPELPKPSISSNNSKPEVDKAVAFCEPEAONTTYLMMV 180
QY 181 NNOSLPVSPRLQLSNGNRTLTLFNVTRNDARAVYCGIQNSVANSRSDPVTLDVLYGPDPTIISP 240
Db 181 NNOSLPVSPRLQLSNGNRTLTLFNVTRNDARAVYCGIQNSVANSRSDPVTLDVLYGPDPTIISP 240
QY 241 TISPLNTSYRSGENLNLSCSHASNPAPQYSWVNGTFOOSTOELFIPNITVNNSGSYTCQ 300
Db 241 TISPLNTSYRSGENLNLSCSHASNPAPQYSWVNGTFOOSTOELFIPNITVNNSGSYTCQ 300
QY 301 AHNSTGLNRTTIVTTTVAEPPKPTITSNNSNPVEDEDAVALTCEPEIQNTTYLMMVNN 360
Db 301 AHNSTGLNRTTIVTTTVAEPPKPTITSNNSNPVEDEDAVALTCEPEIQNTTYLMMVNN 360
QY 361 QSLPVPRLQLSNDNRTLTLSTVRNDVGPYEGCIGNELSVHSDVILNLVXGPDPTI 420
Db 361 QSLPVPRLQLSNDNRTLTLSTVRNDVGPYEGCIGNELSVHSDVILNLVXGPDPTI 420

QY 421 SPSYTYRPGVNLISLSCHAASNPAPQYSMLIDGNIQHTOELFISNTEKNSGLTYCOAN 480
Db 233 ----- 232
QY 481 NSAGSHSRTTYKTTIVSAELPKPSISSNNSKPEVDKAVAFCEPEAONTTYLMMVNGOS 540
Db 233 ----- 232
QY 541 LPVSPRLQLSNGNRTLTLFNVTRNDARAVYCGIQNSVANSRSDPVTLDVLYGPDPTIISP 600
Db 233 ----- 244
QY 601 PDSSYLSGANLNLSCSHASNPSPQYSWRINGIPQOHTOVLFLAKITPNNNGTYACFVSNL 660
Db 245 PDSSYLSGANLNLSCSHASNPSPQYSWRINGIPQOHTOVLFLAKITPNNNGTYACFVSNL 304
QY 661 ATGRNNSIVKSIIVTSASGTSPLSAGATVGMIGVLGVVALI 702
Db 305 ATGRNNSIVKSIIVTSASGTSPLSAGATVGMIGVLGVVALI 346

RESULT 15
US-11-080-991-4
; Sequence 4, Application US/11080991
; Publication No. US2005026437A1
; GENERAL INFORMATION:
; APPLICANT: Velby, Peter Ole
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
; FILE REFERENCE: MRI-039
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US/10/176,847
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-080-991-4

Query Match 38.8%; Score 1443; DB 7; Length 344;
Best Local Similarity 83.9%; Pred. No. 1e-83;
Matches 271; Conservative 11; Mismatches 41; Indels 0; Gaps 0;
QY 1 MESPSAPPHRMCTPMQRLTLTASLTFMNPPTAKLTITESTPPNVAEGKEVLLVHNLPQ 60
Db 1 MGPSPAPPCRLHVPKKEVLLTASLTFMNPPTAKLTITESTPPNVAEGKEVLLVHNLPQ 60
QY 61 HLFYGMVYGERVDGNROITIGVIGTQOATPGPAYSGREIITYPNASLLIIONITQNDTGFY 120
Db 61 HLFYGMVYGERVDGNROITIGVIGTQOATPGPAYSGREIITYPNASLLIIONITQNDTGFY 120
QY 121 TLHVIKSDLVNEBAGTQFRVYPELPKPSISSNNSKPEVDKAVAFCEPEAONTTYLMMV 180
Db 121 TLHVIKSDLVNEBAGTQFRVYPELPKPSISSNNSKPEVDKAVAFCEPEAONTTYLMMV 180
QY 181 NNOSLPVSPRLQLSNGNRTLTLFNVTRNDARAVYCGIQNSVANSRSDPVTLDVLYGPDPTIISP 240
Db 181 NNOSLPVSPRLQLSNGNRTLTLFNVTRNDARAVYCGIQNSVANSRSDPVTLDVLYGPDPTIISP 240
QY 241 TISPLNTSYRSGENLNLSCSHASNPAPQYSWVNGTFOOSTOELFIPNITVNNSGSYTCQ 300
Db 241 TISPLNTSYRSGENLNLSCSHASNPAPQYSWVNGTFOOSTOELFIPNITVNNSGSYTCQ 300
QY 301 AHNSTGLNRTTIVTTTVAEPPKPTITSNNSNPVEDEDAVALTCEPEIQNTTYLMMVNN 360
Db 301 AHNSTGLNRTTIVTTTVAEPPKPTITSNNSNPVEDEDAVALTCEPEIQNTTYLMMVNN 360

Search completed: April 10, 2006, 18:13:23

Job time : 27.4851 secs

THIS PAGE LEFT BLANK

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 10, 2006, 18:07:01 ; Search time 51.7426 Seconds
(without alignments)
1121.675 Million cell updates/sec

Title: US-10-734-564-72

Perfect score: 3721

Sequence: 1 MESPSAPHRKICFMRQLL.....LSAGATGICMIGLVGVALI 702

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: Issued Patents AA:*
- 2: /cgn2_6/ptodata/1/1aa/5 COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6 COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/CTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
- 7: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3721	100.0	702	2	US-09-949-016-6484
2	3721	100.0	734	1	US-08-389-459A-17
3	3721	100.0	734	2	US-08-987-867A-17
4	3721	100.0	740	2	US-09-949-016-8168
5	3700	99.4	698	1	US-08-602-725-36
6	3402	91.4	642	1	US-08-217-299-1
7	1600.5	43.0	464	1	US-08-602-725-32
8	1600.5	43.0	464	2	US-09-949-016-6116
9	1600.5	43.0	464	2	US-09-949-016-7525
10	1443	38.8	365	2	US-09-949-016-7591
11	1424	38.3	321	6	5169835-17
12	1415	38.0	344	1	US-08-602-725-34
13	1272	34.2	349	2	US-09-924-103-4
14	1126.5	30.3	419	6	5169835-2
15	1099	29.5	424	6	5169835-6
16	773	20.8	354	6	5169835-4
17	739	19.9	156	2	US-09-370-838-210
18	739	19.9	156	2	US-09-854-133-210
19	667	17.9	248	6	5169835-15
20	635	17.1	141	2	US-09-924-103-2
21	560.5	15.1	230	6	5169835-13
22	505	13.6	92	2	US-09-370-838-211
23	505	13.6	92	2	US-09-854-133-211
24	413.5	11.1	4126	2	US-09-953-096-4
25	413.5	11.1	5518	2	US-09-953-096-2
26	411	11.0	862	2	US-09-949-002-427
27	410	11.0	847	2	US-09-949-002-328

28	402	10.8	144	6	5169835-8	Parent No. 5169835
29	395.5	10.6	4391	2	US-10-006-011A-2	Sequence 2, Appl
30	379	10.2	143	6	5169835-18	Patent No. 5169835
31	362	9.7	1709	2	US-09-949-016-10503	Sequence 10503, A
32	351	9.4	122	6	5169835-12	Patent No. 5169835
33	343	9.2	596	1	US-08-752-307B-13	Sequence 13, Appl
34	343	9.2	596	2	US-09-707-802-13	Sequence 13, Appl
35	343	9.2	596	2	US-09-991-326-13	Sequence 13, Appl
36	317	8.5	607	1	US-08-752-307B-12	Sequence 12, Appl
37	317	8.5	607	2	US-09-707-802-12	Sequence 12, Appl
38	317	8.5	607	2	US-09-991-326-12	Sequence 12, Appl
39	311	8.4	107	2	US-09-513-999C-7818	Sequence 7818, Ap
40	307.5	8.3	848	2	US-09-787-443-44	Sequence 44, Appl
41	303.5	8.2	819	2	US-09-949-016-11044	Sequence 11044, A
42	303	8.1	1381	2	US-09-540-245A-16	Sequence 16, Appl
43	303	8.1	1381	2	US-10-289-776-16	Sequence 16, Appl
44	302.5	8.1	828	1	US-08-261-304-2	Sequence 2, Appl
45	301	8.1	1571	2	US-08-956-991-11	Sequence 11, Appl

ALIGNMENTS

Issued 11/2/04

RESULT 1									
US-09-949-016-6484									
Sequence 6484, Application US/09949016									
Patent No. 6612359									
GENERAL INFORMATION:									
APPLICANT: VENTER, J. Craig et al.									
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED									
FILE REFERENCE: C1001307									
CURRENT FILING DATE: 2000-04-14									
PRIOR APPLICATION NUMBER: 60/241,755									
PRIOR FILING DATE: 2000-10-20									
PRIOR APPLICATION NUMBER: 60/237,768									
PRIOR FILING DATE: 2000-10-03									
PRIOR APPLICATION NUMBER: 60/231,498									
PRIOR FILING DATE: 2000-09-08									
NUMBER OF SEQ ID NOS: 207012									
SOFTWARE: FASTSEQ for Windows Version 4.0									
SEQ ID NO 6484									
LENGTH: 702									
TYPE: PRT									
ORGANISM: Human									
US-09-949-016-6484									
Query Match									
Best local Similarity 100.0%; Score 3721; DB 2; Length 702;									
Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	MESPSAPHRKICFMRQLLTASLLTFNPPYAKLTFTSTPFVNAEKEVLLVHNLPQ	60						
DB	1	MESPSAPHRKICFMRQLLTASLLTFNPPYAKLTFTSTPFVNAEKEVLLVHNLPQ	60						
QY	61	HLFGYSYKGRVDCNRQIIIGYVIGTOATPGAYSGREIITYPNASLLIIONIDTFY	120						
DB	61	HLFGYSYKGRVDCNRQIIIGYVIGTOATPGAYSGREIITYPNASLLIIONIDTFY	120						
QY	121	TLHVKISDLVNEATGQFRVYBELPKPSISNNKPKVEDKQAVAFPCPEPQDATTYLMWV	180						
DB	121	TLHVKISDLVNEATGQFRVYBELPKPSISNNKPKVEDKQAVAFPCPEPQDATTYLMWV	180						
QY	181	NNQSLPVSPRLQISNGRRTLLTFNVTNDTASYKCTQNPVSARRSDVILNLYGPDAP	240						
DB	181	NNQSLPVSPRLQISNGRRTLLTFNVTNDTASYKCTQNPVSARRSDVILNLYGPDAP	240						
QY	241	TISPLNTSYSGENIANTSCAASNPAPQYSFVNGTFOOSTQELPIPIITVNNSGSYTCQ	300						
DB	241	TISPLNTSYSGENIANTSCAASNPAPQYSFVNGTFOOSTQELPIPIITVNNSGSYTCQ	300						
QY	301	AHNSDTGLNRTTITTTITVVAEPKPKFTLSNNSNVEDEDAVALTCEPEIQNTTYLMMWNN	360						

```

|||||
Db 301 AHNSTGLNRTTITTYVAEPPKPFITSNNSNPVEDDAVALTCEPEIQNTTYLMWVNN 360
Qy 361 OSLPVSPRLQSLNDNRRTLLLSVTRNDVGPYECGIONELSDHSDPVLNVLXGPDPTI 420
Db 361 OSLPVSPRLQSLNDNRRTLLLSVTRNDVGPYECGIONELSDHSDPVLNVLXGPDPTI 420
Qy 421 SPSTYTRPGVNLISCHASNPPOAYSWLIDGNIQHTOELFISNTEKNSGLTYCOAN 480
Db 421 SPSTYTRPGVNLISCHASNPPOAYSWLIDGNIQHTOELFISNTEKNSGLTYCOAN 480
Qy 481 NSAGHSRTTYKTIIVSAELPKPSSISNNSKPVEDDAVAFTCEPEAQNTTYLMWVNGS 540
Db 481 NSAGHSRTTYKTIIVSAELPKPSSISNNSKPVEDDAVAFTCEPEAQNTTYLMWVNGS 540
Qy 541 LPVSPRLQSLNDRRTLLFNTRNDARAAYVCGIQNSVSANRSDPVLTVLXGPDPTI 600
Db 541 LPVSPRLQSLNDRRTLLFNTRNDARAAYVCGIQNSVSANRSDPVLTVLXGPDPTI 600
Qy 601 PDSSTYLSGANLNLSCHASNPPOAYSWFVNGTFOOSTOELFIPNITVNNSSGTYCO 300
Db 601 PDSSTYLSGANLNLSCHASNPPOAYSWFVNGTFOOSTOELFIPNITVNNSSGTYCO 332
Qy 661 ATGRNNSIVKSIIVSASGTPGLSAGATVGMIGLVGVALLI 702
Db 661 ATGRNNSIVKSIIVSASGTPGLSAGATVGMIGLVGVALLI 702

RESULT 2
US-08-389-459A-17
; Sequence 17, Application US/08389459A
; Patent No. 581512
; GENERAL INFORMATION:
; APPLICANT: Morrow, Casey D. and Porter, Donna, C.
; TITLE OF INVENTION: ENCAPSIDATED RECOMBINANT POLIOVIRUS
; TITLE OF INVENTION: NUCLEIC ACID AND METHODS OF MAKING AND
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, SUITE 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/389,459A
; FILING DATE: 15-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/087,009
; FILING DATE: 01-JUL-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Silverl, Jean M.
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: UAG-004CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 734 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-389-459A-17

```

```

Query Match      100.0%; Score 3721; DB 1; Length 734;
Best Local Similarity 100.0%; Pred. No. 3e-271;
Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MESPSAPPHRNCIPQORILLTASLLTFWNPPTTAKLTTESTPPNVAEKEVILLVHNPQ 60
Db 33 MESPSAPPHRNCIPQORILLTASLLTFWNPPTTAKLTTESTPPNVAEKEVILLVHNPQ 92
Qy 61 HLFQSWTKGERVDGNROIIGVIGTQOATGPAVSGREIITYPNASLLIONIQNDTFY 120
Db 93 HLFQSWTKGERVDGNROIIGVIGTQOATGPAVSGREIITYPNASLLIONIQNDTFY 152
Qy 121 TLHVSKDLVNEEATGQRYVPELKPSSISNNSKPVEDDAVAFTCEPEAQNTTYLMWV 180
Db 153 TLHVSKDLVNEEATGQRYVPELKPSSISNNSKPVEDDAVAFTCEPEAQNTTYLMWV 212
Qy 181 NNQSLPVSPRLQSLNDRRTLLFNTRNDTASYKETONPVSAKSDVILLNVLXGPDAP 240
Db 213 NNQSLPVSPRLQSLNDRRTLLFNTRNDTASYKETONPVSAKSDVILLNVLXGPDAP 272
Qy 241 TISPLNTSYRSGENLNLSCHASNPPOAYSWFVNGTFOOSTOELFIPNITVNNSSGTYCO 300
Db 273 TISPLNTSYRSGENLNLSCHASNPPOAYSWFVNGTFOOSTOELFIPNITVNNSSGTYCO 332
Qy 301 AHNSTGLNRTTITTYVAEPPKPFITSNNSNPVEDDAVALTCEPEIQNTTYLMWVNN 360
Db 333 AHNSTGLNRTTITTYVAEPPKPFITSNNSNPVEDDAVALTCEPEIQNTTYLMWVNN 392
Qy 361 OSLPVSPRLQSLNDNRRTLLLSVTRNDVGPYECGIONELSDHSDPVLNVLXGPDPTI 420
Db 393 OSLPVSPRLQSLNDNRRTLLLSVTRNDVGPYECGIONELSDHSDPVLNVLXGPDPTI 452
Qy 421 SPSTYTRPGVNLISCHASNPPOAYSWLIDGNIQHTOELFISNTEKNSGLTYCOAN 480
Db 453 SPSTYTRPGVNLISCHASNPPOAYSWLIDGNIQHTOELFISNTEKNSGLTYCOAN 512
Qy 481 NSAGHSRTTYKTIIVSAELPKPSSISNNSKPVEDDAVAFTCEPEAQNTTYLMWVNGS 540
Db 513 NSAGHSRTTYKTIIVSAELPKPSSISNNSKPVEDDAVAFTCEPEAQNTTYLMWVNGS 572
Qy 541 LPVSPRLQSLNDRRTLLFNTRNDARAAYVCGIQNSVSANRSDPVLTVLXGPDPTI 600
Db 573 LPVSPRLQSLNDRRTLLFNTRNDARAAYVCGIQNSVSANRSDPVLTVLXGPDPTI 632
Qy 601 PDSSTYLSGANLNLSCHASNPPOAYSWFVNGTFOOSTOELFIPNITVNNSSGTYCOAN 660
Db 633 PDSSTYLSGANLNLSCHASNPPOAYSWFVNGTFOOSTOELFIPNITVNNSSGTYCOAN 692
Qy 661 ATGRNNSIVKSIIVSASGTPGLSAGATVGMIGLVGVALLI 702
Db 693 ATGRNNSIVKSIIVSASGTPGLSAGATVGMIGLVGVALLI 734

RESULT 3
US-08-987-867A-17
; Sequence 17, Application US/08987867A
; Patent No. 6063384
; GENERAL INFORMATION:
; APPLICANT: C. Morrow et al.
; TITLE OF INVENTION: ENCAPSIDATED RECOMBINANT VIRAL
; TITLE OF INVENTION: NUCLEIC ACID AND METHODS OF MAKING AND
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 STATE STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/987,867A
FILING DATE: 09-DEC-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/087,009
FILING DATE: 01-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: UAP-004CPDV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 734 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-987-867A-17

Query Match 100.0%; Score 3721; DB 2; Length 734;
Best Local Similarity 100.0%; Pred. No. 3e-271;
Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSAPPHRCIPWQRLTLTASLLTFWNPPTAKLTIESPPFVNAEKEVLLVHNLPO 60
DB 33 MESSAPPHRCIPWQRLTLTASLLTFWNPPTAKLTIESPPFVNAEKEVLLVHNLPO 92
QY 61 HLFQSWYKGRVGNRQIIGVIGTQOATGPAVSGBEIIYPNASLLIONIONDITFY 120
DB 93 HLFQSWYKGRVGNRQIIGVIGTQOATGPAVSGBEIIYPNASLLIONIONDITFY 152
QY 121 TLHAIKSDLVNEAATGQFRVYPELPKPSISSNSKPVEDKDAVAFCEPETODATYLMWV 180
DB 153 TLHAIKSDLVNEAATGQFRVYPELPKPSISSNSKPVEDKDAVAFCEPETODATYLMWV 212
QY 181 NNQSLPVSRLQSLNGNRTLLFVTRNDTASYKCETONPVASRRSDSVIILVLYGPDAP 240
DB 213 NNQSLPVSRLQSLNGNRTLLFVTRNDTASYKCETONPVASRRSDSVIILVLYGPDAP 272
QY 241 TISPLANTSYRGENMLNSCHASNPAPQYSWFVNGTFOOSTOELFIPITVNNSGSYTCQ 300
DB 273 TISPLANTSYRGENMLNSCHASNPAPQYSWFVNGTFOOSTOELFIPITVNNSGSYTCQ 332
QY 301 AHNSDTGILNRTTITTYAEPKPKFITSNNSNPVEDDAVALTCBEPIONTTYLLMMVNN 360
DB 333 AHNSDTGILNRTTITTYAEPKPKFITSNNSNPVEDDAVALTCBEPIONTTYLLMMVNN 392
QY 361 QSLPVSRLQSLNDNRRTLLSVTRNDVGYECCIGNELSYDHSDPVILVLYGPDPTI 420
DB 393 QSLPVSRLQSLNDNRRTLLSVTRNDVGYECCIGNELSYDHSDPVILVLYGPDPTI 452
QY 421 SPSTYTYRPGVNLSSLCHASNPAPQYSWMLIDGNIQOHTOELFISNTEKNSGLYTCQAN 480
DB 453 SPSTYTYRPGVNLSSLCHASNPAPQYSWMLIDGNIQOHTOELFISNTEKNSGLYTCQAN 512
QY 481 NSASGHSRTTYKTTTVAELPKPSISSNSKPVEDKDAVAFCEPEAONTTYLLMMVNGOS 540
DB 513 NSASGHSRTTYKTTTVAELPKPSISSNSKPVEDKDAVAFCEPEAONTTYLLMMVNGOS 572
QY 541 LPVSPRLQSLNGNRTLLFVTRNDARAYVCGIONSVSANRSDPTLLDVLVYGPDPPIISP 600
DB 573 LPVSPRLQSLNGNRTLLFVTRNDARAYVCGIONSVSANRSDPTLLDVLVYGPDPPIISP 632
QY 601 PDSSYLGANINLSCHASNPSPQYSWRINGIPOOHTOVLFIKTTTPNNNGTYACFVSNL 660
DB 633 PDSSYLGANINLSCHASNPSPQYSWRINGIPOOHTOVLFIKTTTPNNNGTYACFVSNL 692
QY 661 ATGRNNSIVKSIIVSASGTSRGLSAGATVGMIGVGVALLI 702

DB 693 ATGRNNSIVKSIIVSASGTSRGLSAGATVGMIGVGVALLI 734

RESULT 4
US-09-949-016-8168
Sequence 8168, Application US/09949016
Patent No. 6812319
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8168
LENGTH: 740
TYPE: PRT
ORGANISM: Human
US-09-949-016-8168

Query Match 100.0%; Score 3721; DB 2; Length 740;
Best Local Similarity 100.0%; Pred. No. 3.1e-271;
Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSAPPHRCIPWQRLTLTASLLTFWNPPTAKLTIESPPFVNAEKEVLLVHNLPO 60
DB 39 MESSAPPHRCIPWQRLTLTASLLTFWNPPTAKLTIESPPFVNAEKEVLLVHNLPO 98
QY 61 HLFQSWYKGRVGNRQIIGVIGTQOATGPAVSGBEIIYPNASLLIONIONDITFY 120
DB 99 HLFQSWYKGRVGNRQIIGVIGTQOATGPAVSGBEIIYPNASLLIONIONDITFY 158
QY 121 TLHAIKSDLVNEAATGQFRVYPELPKPSISSNSKPVEDKDAVAFCEPETODATYLMWV 180
DB 159 TLHAIKSDLVNEAATGQFRVYPELPKPSISSNSKPVEDKDAVAFCEPETODATYLMWV 218
QY 181 NNQSLPVSRLQSLNGNRTLLFVTRNDTASYKCETONPVASRRSDSVIILVLYGPDAP 240
DB 219 NNQSLPVSRLQSLNGNRTLLFVTRNDTASYKCETONPVASRRSDSVIILVLYGPDAP 278
QY 241 TISPLANTSYRGENMLNSCHASNPAPQYSWFVNGTFOOSTOELFIPITVNNSGSYTCQ 300
DB 279 TISPLANTSYRGENMLNSCHASNPAPQYSWFVNGTFOOSTOELFIPITVNNSGSYTCQ 338
QY 301 AHNSDTGILNRTTITTYAEPKPKFITSNNSNPVEDDAVALTCBEPIONTTYLLMMVNN 360
DB 339 AHNSDTGILNRTTITTYAEPKPKFITSNNSNPVEDDAVALTCBEPIONTTYLLMMVNN 398
QY 361 QSLPVSRLQSLNDNRRTLLSVTRNDVGYECCIGNELSYDHSDPVILVLYGPDPTI 420
DB 399 QSLPVSRLQSLNDNRRTLLSVTRNDVGYECCIGNELSYDHSDPVILVLYGPDPTI 458
QY 421 SPSTYTYRPGVNLSSLCHASNPAPQYSWMLIDGNIQOHTOELFISNTEKNSGLYTCQAN 480
DB 459 SPSTYTYRPGVNLSSLCHASNPAPQYSWMLIDGNIQOHTOELFISNTEKNSGLYTCQAN 518
QY 481 NSASGHSRTTYKTTTVAELPKPSISSNSKPVEDKDAVAFCEPEAONTTYLLMMVNGOS 540
DB 519 NSASGHSRTTYKTTTVAELPKPSISSNSKPVEDKDAVAFCEPEAONTTYLLMMVNGOS 578
QY 541 LPVSPRLQSLNGNRTLLFVTRNDARAYVCGIONSVSANRSDPTLLDVLVYGPDPPIISP 600
DB 579 LPVSPRLQSLNGNRTLLFVTRNDARAYVCGIONSVSANRSDPTLLDVLVYGPDPPIISP 638

Qy	Db	Qy	Db
60	639	661	699
PDSSYLSGALNLTNSCHSASNPQVSMRNLNGIPQOHTOVLFLAKTTPNNNGTACFVSNL	PDSSYLSGALNLTNSCHSASNPQVSMRNLNGIPQOHTOVLFLAKTTPNNNGTACFVSNL	ATGRNNSIVSITVSASGTSFGISAGATGIMIGVLVGYALI	ATGRNNSIVSITVSASGTSFGISAGATGIMIGVLVGYALI
660	699	702	740
PDSSYLSGALNLTNSCHSASNPQVSMRNLNGIPQOHTOVLFLAKTTPNNNGTACFVSNL	PDSSYLSGALNLTNSCHSASNPQVSMRNLNGIPQOHTOVLFLAKTTPNNNGTACFVSNL	ATGRNNSIVSITVSASGTSFGISAGATGIMIGVLVGYALI	ATGRNNSIVSITVSASGTSFGISAGATGIMIGVLVGYALI

RESULT 5

US-08-602-725-36
Sequence 36, Application US/06602725
Patent No. 5965710
GENERAL INFORMATION:
APPLICANT: BODMER, WALTER F
APPLICANT: DURBIN, HELGA
APPLICANT: SNARY, DAVID
APPLICANT: STEWART, LORNA MD
APPLICANT: YOUNG, SUSAN
APPLICANT: BATES, PAUL A
TITLE OF INVENTION: MONOCLONAL ANTIBODIES FOR USE IN
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF COLORECTAL CANCER
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESSES:
ADDRESSEE: NIXON & VANDERHIVE P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/602,725
FILING DATE: 02-FEB-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB94/01816
FILING DATE: 19-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9317423
FILING DATE: 21-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36653
REFERENCE/DOCKET NUMBER: 1090-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4091
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 698 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-602-725-36

Query Match	99.4%	Score 3700	DB 1	Length 698
Best Local Similarity	100.0%	Pred. No. 1.1e-269		
Matches 698	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY 5 SAPPHRMCI PMORLLTALITFENNPPTAKLITESTPEVNAEGKEVLLVHNLPHLFC 64

Db 1 SAPPHRMCI PMORLLTALITFENNPPTAKLITESTPEVNAEGKEVLLVHNLPHLFC 60

QY YSMYGERDNGRROIIGYIGTQADPGPAGSRELIIPASLLIIONIDGFTIHY 124

QY YSMYGERDNGRROIIGYIGTQADPGPAGSRELIIPASLLIIONIDGFTIHY 120

QY 61 YSMYGERDNGRROIIGYIGTQADPGPAGSRELIIPASLLIIONIDGFTIHY 120

QY 125 IKSDLVNEBTAQGFRRVYPELPKPSISSNNKSPVEDKDAVAFTCEPTQDATYILMVNNOS 184

Dd	121	IKSDLVNBEATQGFRRYPBEPKPSISSNNSKRPVEDKXAVATCEPERFDQATYLMWVNNOS	186
Oy	185	LPVSPRLQJNSGNRRITLTFNTRNDTASYKCETONPVSARRSDSVILNLVYGPDAPIITSP	244
Dd	181	LPVSPRLQJNSGNRRITLTFNTRNDTASAKCETONPVSARRSDSVILNLVYGPDAPIITSP	240
Oy	245	LNTSYSGENLNLSCHAASNPPAOYSWFNPGNPOOSTOELRIPNITVNNSGSYCOAHNS	304
Dd	241	LNTSYSGENLNLSCHAASNPPAOYSWFNPGTFQOSTOELRIPNITVNNSGSYCOAHNS	300
Oy	305	DTGLNRTVYITTVYAEPPKPIITSNNSNPVEDBAVALTCEPEIONTYLLMWVNNOSLP	364
Dd	301	DTGLNRTVYITTVYAEPPKPIITSNNSNPVEDBAVALTCEPEIONTYLLMWVNNOSLP	360
Oy	365	VSPRLQJNSDNRITLLTLSTTRNDVCPYECGIONELSVHSDPVLNLVYGPDDPTISPSY	424
Dd	361	VSPRLQJNSDNRITLLTLSTTRNDVCPYECGIONELSVHSDPVLNLVYGPDDPTISPSY	420
Oy	425	TYPRPGVNLISLSCHAASNPPAOYSWLIQGNIOQHTQBELFISNITEKNSGLTQCOANNSAS	484
Dd	421	TYPRPGVNLISLSCHAASNPPAOYSWLIQGNIOQHTQBELFISNITEKNSGLTQCOANNSAS	480
Oy	485	GHSRTTYKTIITVSAELPKPSSISNNSKRPVEDKXAVATCEPEAONTYLLMWVNNOSLPVS	544
Dd	481	GHSRTTYKTIITVSAELPKPSSISNNSKRPVEDKXAVATCEPEAONTYLLMWVNNOSLPVS	540
Oy	545	PRLOJNSGNRRITLLFNTRNDARAYVCGIQNSVSNRSDPVTLLVYXGPDPIITSPDSS	604
Dd	541	PRLOJNSGNRRITLLFNTRNDARAYVCGIQNSVSNRSDPVTLLVYXGPDPIITSPDSS	600
Oy	605	YLSGANLNLSCHASNPSPQYSWRINGIPQOHTQVLFIAKITPPNNGTACFVSNLATGR	664
Dd	601	YLSGANLNLSCHASNPSPQYSWRINGIPQOHTQVLFIAKITPPNNGTACFVSNLATGR	660
Oy	665	NNSIVXSITVYASGTSPIGSAGATGIMIGVLVGYALI 702	
Dd	661	NNSIVXSITVYASGTSPIGSAGATGIMIGVLVGYALI 698	

RESULT 6

```

US-08-217-299-1
:
: Sequence 1, Application US/08217299
: Patent No. 5672513
:
: GENERAL INFORMATION:
:
: APPLICANT: Mach, J. P.
: APPLICANT: Peligrin, A.
: APPLICANT: Terasaki, A.
:
: TITLE OF INVENTION: Carcinoembryonic Antigen Derivatives
:
: NUMBER OF SEQUENCES: 4
:
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Hoffmann-La Roche Inc.
: STREET: 340 Kingsland Street
: CITY: Nutley
:
: STATE: NJ
:
: COUNTRY: USA
:
: ZIP: 07110
:
: COMPUTER READABLE FORM:
:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
:
: CURRENT APPLICATION DATA:
:
: APPLICATION NUMBER: US/08/217,299
:
: FILING DATE:
:
: CLASSIFICATION: 435
:
: PRIOR APPLICATION DATA:
:
: APPLICATION NUMBER: EP 93810214.2
:
: FILING DATE: 25-MAR-1993
:
: ATTORNEY/AGENT INFORMATION:
:
: NAME: Pokras, Bruce A.
:
: REGISTRATION NUMBER: 32,748
:
: REFERENCE/DOCKET NUMBER: RAN 4093/096
:

```

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (201) 235-5801
 TELEFAX: (201) 235-3500
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 642 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 HYPOTHEICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: C-terminal
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 US-08-217-299-1

Query Match 91.4%; Score 3402; DB 1; Length 642;
 Best Local Similarity 100.0%; Pred. No. 2,4e-247;
 Matches 642; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 KLITESTPENVAEKGVLLVHNLPOHLFGYSWYKGEVDGNRQITGVIGTQATPGPA 94
 DB 1 KLITESTPENVAEKGVLLVHNLPOHLFGYSWYKGEVDGNRQITGVIGTQATPGPA 60
 QY 95 YSGREIIPYNASLIIONIDTGYTLHVKSDLVNEEATGQPRVPELEKPSISNNS 154
 DB 61 YSGREIIPYNASLIIONIDTGYTLHVKSDLVNEEATGQPRVPELEKPSISNNS 120
 QY 155 KPVEDKDAVAFTCEPETODATYLMWVNNOSLPVSPRLQLSNGNRTLTFFNTRNDTASYK 214
 DB 121 KPVEDKDAVAFTCEPETODATYLMWVNNOSLPVSPRLQLSNGNRTLTFFNTRNDTASYK 180
 QY 215 CETNPVSARSDSVILNVLGPDAPITSPANTSYRSGENINLSCHAASNPAPQYSWFVN 274
 DB 181 CETNPVSARSDSVILNVLGPDAPITSPANTSYRSGENINLSCHAASNPAPQYSWFVN 240
 QY 275 GTFOOSTOELFIPNITVNNSGSYTQAHNSDTGLNRTVTITTYAEPKPEITSNNSNP 334
 DB 241 GTFOOSTOELFIPNITVNNSGSYTQAHNSDTGLNRTVTITTYAEPKPEITSNNSNP 300
 QY 335 VEDEDAVALTCERPEIQTYYLWVNNOSLPVSPRLQLSNGNRTLTFFNTRNDTASYK 394
 DB 301 VEDEDAVALTCERPEIQTYYLWVNNOSLPVSPRLQLSNGNRTLTFFNTRNDTASYK 360
 QY 395 IONELSYDHSDPVILNVLGPDPTISPSYTYRPGVNLSSCHAASNPAPQYSWMLDGN 454
 DB 361 IONELSYDHSDPVILNVLGPDPTISPSYTYRPGVNLSSCHAASNPAPQYSWMLDGN 420
 QY 455 IOQTOELFISNTEKNSGLTTCOANNSASGHSRTTYKTTIVSAELPRPSSISNNSKPYE 514
 DB 421 IOQTOELFISNTEKNSGLTTCOANNSASGHSRTTYKTTIVSAELPRPSSISNNSKPYE 480
 QY 515 DKDAVAFTCEPEAQNTTYLWVNNOSLPVSPRLQLSNGNRTLTFFNTRNDTASYK 574
 DB 481 DKDAVAFTCEPEAQNTTYLWVNNOSLPVSPRLQLSNGNRTLTFFNTRNDTASYK 540
 QY 575 NSVSANRSDPYTLNVLGPDPTIISPPDSYLSGANINLSCHAASNPAPQYSWMLDGN 634
 DB 541 NSVSANRSDPYTLNVLGPDPTIISPPDSYLSGANINLSCHAASNPAPQYSWMLDGN 600
 QY 635 OHQOVLFIAKTTNNNTYACFVSNLATGRNNSIVKSIIVSA 676
 DB 601 OHQOVLFIAKTTNNNTYACFVSNLATGRNNSIVKSIIVSA 642

RESULT 7
 US-08-602-725-32
 ; Sequence 32; Application US/08602725
 ; Patent No. 5965710
 ; GENERAL INFORMATION:
 ; APPLICANT: BODMER, WALTER F
 ; APPLICANT: DUBBIN, HEUGA

APPLICANT: SNARY, DAVID
 APPLICANT: STEWART, LORNA MD
 APPLICANT: YOUNG, SUSAN
 APPLICANT: BATES, PAUL A
 TITLE OF INVENTION: MONOCLONAL ANTIBODIES FOR USE IN
 TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF COLORECTAL CANCER
 NUMBER OF SEQUENCES: 40
 CORRESPONDENCE ADDRESS:
 ADDRESSER: NIXON & VANDERHAYE P.C.
 STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
 CITY: ARLINGTON
 STATE: VA
 COUNTRY: USA
 ZIP: 22201
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/602,725
 FILING DATE: 02-FEB-1996
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/GB94/01816
 FILING DATE: 19-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9317423
 FILING DATE: 21-AUG-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: SADOFF, B.J.
 REGISTRATION NUMBER: 36663
 REFERENCE/DOCKET NUMBER: 1090-8
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-816-4091
 TELEFAX: 703-816-4100
 INFORMATION FOR SEQ ID NO: 32:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 464 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-602-725-32

Query Match 43.0%; Score 1600.5; DB 1; Length 464;
 Best Local Similarity 73.0%; Pred. No. 4.3e-112;
 Matches 309; Conservative 30; Mismatches 79; Indels 5; Gaps 2;

QY 5 SAPHRMCIPQORLLTASLITFNNPPTAKLTETSPFNVAEKEVLLVHNLPOHLFG 64
 DB 5 SAPHRMCIPQORLLTASLITFNNPPTAKLTETSPFNVAEKEVLLVHNLPOHLFG 64
 QY 65 YSWYKGEVVDGNRQITGVIGTQATPGPAVSGREIIPYNASLIIONIDTGYTLHVK 124
 DB 65 YSWYKGEVVDGNRQITGVIGTQATPGPAVSGREIIPYNASLIIONIDTGYTLHVK 124
 QY 125 IKSDELVEEATGQPRVPELEKPSISNNSKPYEDKDAVAFTCEPETODATYLMWVNNOS 184
 DB 125 IKSDELVEEATGQPRVPELEKPSISNNSKPYEDKDAVAFTCEPETODATYLMWVNNOS 184
 QY 185 LPVSPRLQLSNGNRTLTFFNTRNDTASYCENONPVSAERSDSVILNVLGPDPTISP 244
 DB 185 LPVSPRLQLSNGNRTLTFFNTRNDTASYCENONPVSAERSDSVILNVLGPDPTISP 244
 QY 245 LNTSYRSGENINLSCHAASNPAPQYSWMLDGNFIPNITVNNSGSYTQAHNS 304
 DB 245 LNTSYRSGENINLSCHAASNPAPQYSWMLDGNFIPNITVNNSGSYTQAHNS 304
 QY 305 DTGLNRTVTITTYAEPKPEITSNNSNPVEDDAVALTCERPEIQTYYLWVNNOS 361
 DB 305 DTGLNRTVTITTYAEPKPEITSNNSNPVEDDAVALTCERPEIQTYYLWVNNOS 361
 QY 362 SLVSPRLQLSNGNRTLTFFNTRNDTASYCENONPVSAERSDSVILNVLGPDPTISP 419

```
DB 365 SLPSSEKMLSGCNTLLTSLNPKVEDAGTYWCEVFNPSKNSDPTMLNVTNALPQENG 424
QY 420 ISP 422
DB 425 LSP 427

RESULT 8
US-09-949-016-6116
; Sequence 6116; Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6116
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6116

Query Match 43.0%; Score 1600.5; DB 2; Length 464;
Best Local Similarity 73.0%; Pred. No. 4.3e-112;
Matches 309; Conservative 30; Mismatches 79; Indels 5; Gaps 2;

QY 5 SAPPHRMCIPMORLLTTLTASLTFMNPPTAKLTISTEPFNVAEGKEVLLVHNLPOHLFG 64
DB 5 SAPLHRVVPWOGCLLTSLTFTMNPPTTAQLTSTMPFNVAEGKEVLLVHNLPOHLFG 64
QY 65 YSMYGERVDGNRQIIGVYIGTQATPGPAYSGREIIPNASLLIQNIIONDTGFTYTLHV 124
DB 65 YSMYGERVDGNRQIIGVYIGTQATPGPAYSGREIIPNASLLIQNIIONDTGFTYTLHV 124
QY 125 IKSDLVNEBATGQFHYVPELPKPSISSNNSNPVEDKDAVAFCEPETDPTTYLMMINNS 184
DB 125 IKSDLVNEBATGQFHYVPELPKPSISSNNSNPVEDKDAVAFCEPETDPTTYLMMINNS 184
QY 185 LPVSPRLQSLNGNRLLTFLNVTNRNDTASYKCEIOPNSARSDSVILNVLVGPDAPTISP 244
DB 185 LPVSPRLQSLNGNRLLTFLNVTNRNDTASYKCEIOPNSARSDSVILNVLVGPDAPTISP 244
QY 185 LVSFPRLOSLNGNRLLTFLNVTNRNDTASYKCEIOPNSARSDSVILNVLVGPDAPTISP 244
DB 185 LVSFPRLOSLNGNRLLTFLNVTNRNDTASYKCEIOPNSARSDSVILNVLVGPDAPTISP 244
QY 245 LNTSYRSGENLMSCHAASNPAPQYSWFGNGTFOGSTOELFIPNITVNNSGSYTCOAHNS 304
DB 245 LNTSYRSGENLMSCHAASNPAPQYSWFGNGTFOGSTOELFIPNITVNNSGSYTCOAHNS 304
QY 245 SDTYRRPGANLISLSCYAASNPAPQYSWFGNGTFOGSTOELFIPNITVNNSGSYTCOAHNS 304
DB 245 SDTYRRPGANLISLSCYAASNPAPQYSWFGNGTFOGSTOELFIPNITVNNSGSYTCOAHNS 304
QY 305 DTGLARTTYTITTYVAEPP---KPFITSNNSNPVEDKDAVAFCEPETDPTTYLMMINNS 361
DB 305 DTGLARTTYTITTYVAEPP---KPFITSNNSNPVEDKDAVAFCEPETDPTTYLMMINNS 361
QY 362 SLPSVPRLOSLNDNRLLTFLNVTNRNDTASYKCEIOPNSARSDSVILNVLVGPDAPTISP 419
DB 362 SLPSVPRLOSLNDNRLLTFLNVTNRNDTASYKCEIOPNSARSDSVILNVLVGPDAPTISP 419
QY 365 SLPSSEKMLSGCNTLLTSLNPKVEDAGTYWCEVFNPSKNSDPTMLNVTNALPQENG 424
DB 365 SLPSSEKMLSGCNTLLTSLNPKVEDAGTYWCEVFNPSKNSDPTMLNVTNALPQENG 424

QY 420 ISP 422
DB 425 LSP 427

RESULT 9
US-09-949-016-7525
; Sequence 7525; Application US/09949016
```

```
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7525
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7525

Query Match 43.0%; Score 1600.5; DB 2; Length 464;
Best Local Similarity 73.0%; Pred. No. 4.3e-112;
Matches 309; Conservative 30; Mismatches 79; Indels 5; Gaps 2;

QY 5 SAPPHRMCIPMORLLTTLTASLTFMNPPTAKLTISTEPFNVAEGKEVLLVHNLPOHLFG 64
DB 5 SAPLHRVVPWOGCLLTSLTFTMNPPTTAQLTSTMPFNVAEGKEVLLVHNLPOHLFG 64
QY 65 YSMYGERVDGNRQIIGVYIGTQATPGPAYSGREIIPNASLLIQNIIONDTGFTYTLHV 124
DB 65 YSMYGERVDGNRQIIGVYIGTQATPGPAYSGREIIPNASLLIQNIIONDTGFTYTLHV 124
QY 125 IKSDLVNEBATGQFHYVPELPKPSISSNNSNPVEDKDAVAFCEPETDPTTYLMMINNS 184
DB 125 IKSDLVNEBATGQFHYVPELPKPSISSNNSNPVEDKDAVAFCEPETDPTTYLMMINNS 184
QY 185 LPVSPRLQSLNGNRLLTFLNVTNRNDTASYKCEIOPNSARSDSVILNVLVGPDAPTISP 244
DB 185 LPVSPRLQSLNGNRLLTFLNVTNRNDTASYKCEIOPNSARSDSVILNVLVGPDAPTISP 244
QY 245 LNTSYRSGENLMSCHAASNPAPQYSWFGNGTFOGSTOELFIPNITVNNSGSYTCOAHNS 304
DB 245 LNTSYRSGENLMSCHAASNPAPQYSWFGNGTFOGSTOELFIPNITVNNSGSYTCOAHNS 304
QY 245 SDTYRRPGANLISLSCYAASNPAPQYSWFGNGTFOGSTOELFIPNITVNNSGSYTCOAHNS 304
DB 245 SDTYRRPGANLISLSCYAASNPAPQYSWFGNGTFOGSTOELFIPNITVNNSGSYTCOAHNS 304
QY 305 DTGLARTTYTITTYVAEPP---KPFITSNNSNPVEDKDAVAFCEPETDPTTYLMMINNS 361
DB 305 DTGLARTTYTITTYVAEPP---KPFITSNNSNPVEDKDAVAFCEPETDPTTYLMMINNS 361
QY 362 SLPSVPRLOSLNDNRLLTFLNVTNRNDTASYKCEIOPNSARSDSVILNVLVGPDAPTISP 419
DB 362 SLPSVPRLOSLNDNRLLTFLNVTNRNDTASYKCEIOPNSARSDSVILNVLVGPDAPTISP 419
QY 365 SLPSSEKMLSGCNTLLTSLNPKVEDAGTYWCEVFNPSKNSDPTMLNVTNALPQENG 424
DB 365 SLPSSEKMLSGCNTLLTSLNPKVEDAGTYWCEVFNPSKNSDPTMLNVTNALPQENG 424

QY 420 ISP 422
DB 425 LSP 427

RESULT 10
US-09-949-016-7591
; Sequence 7591; Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
```

; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 7591
 ; LENGTH: 365
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-09-949-016-7591

Query Match 38.8%; Score 1443; DB 2; Length 365;
 Best Local Similarity 83.9%; Pred. No. 2.1e-100;
 Matches 271; Conservative 11; Mismatches 41; Indels 0; Gaps 0;

QY 1 MESPSAPHRMCIPWRLTLTASLLTFWNPPTAKLTIESTPFNVASKEVLLVHNLPO 60
 DB 22 MGPSAPPCRLHVPKKEVLLTASLLTFWNPPTAKLTIESTPFNVASKEVLLVHNLPO 81
 QY 61 HLFQSWYKGERVDGNRQIIIGYVIGTQOATPGPAYSGRETIYPNASLLIQNTDNGFY 120
 DB 82 NRIGISWYKGERVDGNLSLIVGYVIGTQOATPGPAYSGRETIYPNASLLIQNTDNGFY 141
 QY 121 TLHVTKSDLVNBEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFCEPETQDATYLMWV 180
 DB 142 TLQVTKSDLVNBEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFCEPETQDATYLMWV 201
 QY 181 NNQSLPVSPRLQSLNGNRTTLTFVNTNDTASVYKCEIYNPVASRRSDVILLNVLYGPDAP 240
 DB 202 NGQSLPVSPRLQSLNGNRTTLTFVNTNDTASVYKCEIYNPVASRRSDVILLNVLYGPDAP 261
 QY 241 TISPLNTSYRSGENLNLSCHASNPPAQSFWNGTFOQSTOELFIPNITVNNSSGYTCQ 300
 DB 262 TISSKAKYRSGENLNLSCHASNPPAQSFWNGTFOQSTOELFIPNITVNNSSGYTCQ 321
 QY 301 AHNSDTGLNRTTIVVYAEPP 323
 DB 322 AHNATGNTTIVVYAEPP 344

RESULT 11
 5169835-17
 ; Patent No. 5169835
 ; APPLICANT: WAI-YEE, CHAN
 ; TITLE OF INVENTION: PREGNANCY SPECIFIC PROTEINS APPLICATIONS
 ; NUMBER OF SEQUENCES: 48
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/390,409
 ; FILING DATE: 07-AUG-1989
 ; SEQ ID NO: 17:
 ; LENGTH: 321
 ; 5169835-17

Query Match 38.3%; Score 1424; DB 6; Length 321;
 Best Local Similarity 84.3%; Pred. No. 4.7e-99;
 Matches 268; Conservative 13; Mismatches 37; Indels 0; Gaps 0;

QY 1 MESPSAPHRMCIPWRLTLTASLLTFWNPPTAKLTIESTPFNVASKEVLLVHNLPO 60
 DB 1 MGPSAPPCRLHVPKKEVLLTASLLTFWNPPTAKLTIESTPFNVASKEVLLVHNLPO 60
 QY 61 HLFQSWYKGERVDGNRQIIIGYVIGTQOATPGPAYSGRETIYPNASLLIQNTDNGFY 120
 DB 61 NRIGISWYKGERVDGNLSLIVGYVIGTQOATPGPAYSGRETIYPNASLLIQNTDNGFY 120
 QY 121 TLHVTKSDLVNBEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFCEPETQDATYLMWV 180
 DB 121 TLQVTKSDLVNBEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFCEPETQDATYLMWV 180
 QY 181 NNQSLPVSPRLQSLNGNRTTLTFVNTNDTASVYKCEIYNPVASRRSDVILLNVLYGPDAP 240
 DB 181 NNQSLPVSPRLQSLNGNRTTLTFVNTNDTASVYKCEIYNPVASRRSDVILLNVLYGPDAP 240

QY 241 TISPLNTSYRSGENLNLSCHASNPPAQSFWNGTFOQSTOELFIPNITVNNSSGYTCQ 300
 DB 241 TISPSDIYRPGANLISCVASNPAPQSWLNGTFOQSTOELFIPNITVNNSSGYTCQ 300
 QY 301 AHNSDTGLNRTTIVVYAEPP 323
 DB 301 AHNATGNTTIVVYAEPP 344

RESULT 12
 US-08-602-725-34
 ; Sequence 34, Application US/08602725
 ; Patent No. 5965710
 ; GENERAL INFORMATION:

; APPLICANT: BODMER, WALTER F
 ; APPLICANT: DURBIN, HELGA
 ; APPLICANT: SNARY, DAVID
 ; APPLICANT: STEWART, LORNA MD
 ; APPLICANT: YOUNG, SUSAN
 ; APPLICANT: BATES, PAUL A
 ; TITLE OF INVENTION: MONOCLONAL ANTIBODIES FOR USE IN
 ; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF COLORECTAL CANCER
 ; NUMBER OF SEQUENCES: 40
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: NIXON & VANDERHAYE P.C.
 ; STREET: 1100 NORTH GUEBE ROAD, 8TH FLOOR
 ; CITY: ARLINGTON
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22201

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/602,725
 ; FILING DATE: 02-FEB-1996
 ; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/GB94/01816
 ; FILING DATE: 19-AUG-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 9317423
 ; FILING DATE: 21-AUG-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: SADOFF, B. J.
 ; REGISTRATION NUMBER: 36663
 ; REFERENCE/DOCKET NUMBER: 1090-8
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-816-4100
 ; TELEFAX: 703-816-4091
 ; INFORMATION FOR SEQ ID NO: 34:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 344 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-602-725-34

Query Match 38.0%; Score 1415; DB 1; Length 344;
 Best Local Similarity 82.7%; Pred. No. 2.5e-98;
 Matches 267; Conservative 12; Mismatches 44; Indels 0; Gaps 0;

QY 1 MESPSAPHRMCIPWRLTLTASLLTFWNPPTAKLTIESTPFNVASKEVLLVHNLPO 60
 DB 1 MGPSAPPCRLHVPKKEVLLTASLLTFWNPPTAKLTIESTPFNVASKEVLLVHNLPO 60
 QY 61 HLFQSWYKGERVDGNRQIIIGYVIGTQOATPGPAYSGRETIYPNASLLIQNTDNGFY 120
 DB 61 NRIGISWYKGERVDGNLSLIVGYVIGTQOATPGPAYSGRETIYPNASLLIQNTDNGFY 120
 QY 121 TLHVTKSDLVNBEATGQFRVYPELPKPSISSNNSKPVEDKDAVAFCEPETQDATYLMWV 180

```
DB 121 TLQVTKSDLVNBEATGQFHVYPELPEKPSISSNNNSPVEDKDAVAFCEPEVQNTTYVMWV 180
QY 181 NNQSLPVSPRLQSLNSGNRTLTLPNTTRNDTASYKCEQONPVARSDSYILNVLYGPDAP 240
DB 181 NNQSLPVSPRLQSLNSGNMTLTLLSVKRDAGSYECEIQNPASANSDDPVTLLNVLYGPDAP 240
QY 241 TISPLNTSYRSGENILNSCHASNPAPQYSWFVNGTFOOSTOELFIPNTTVNNSGSGYTCC 300
DB 241 TISPKANVRPGENILNSCHASNPAPQYSWFVNGTFOOSTOELFIPNTTVNNSGSGYTCC 300
QY 301 AANSDTGLNRTTYTITTYAAPP 323
DB 301 AANSDTGLNRTTYTITTYAAPP 323

RESULT 13
US-09-924-103-4
; Sequence 4, Application US/09924103
; Patent No. 6759045
; GENERAL INFORMATION:
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: HANSEN, HANS J.
; TITLE OF INVENTION: IMMUNOTHERAPY FOR CHRONIC MYELOCYTIC LEUKEMIA
; FILE REFERENCE: 018733-1055
; CURRENT APPLICATION NUMBER: US/09/924,103
; CURRENT FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-924-103-4
```

```
Query Match 34.2%; Score 1272; DB 2; Length 349;
Best Local Similarity 76.8%; Pred. No. 1.4e-87;
Matches 241; Conservative 19; Mismatches 54; Indels 0; Gaps 0;

QY 5 SAPPHRWCIPMORLLITASLITFMNPTTAKLTISTEPFNVAEGKVLVNLPHLFG 64
DB 5 SAPSCMRIPMORLLITASLITFMNPTTAKLTISTEPFNVAEGKVLVNLPHLFG 64
QY 65 YSMYGERVDGNROIGVIGTQATPGPAYSGREIIPNASLLIIONIDTGFYTLHV 124
DB 65 YMYKGETVDANRIIGVYISNOQITPGPAYSGREIIPNASLLIIONIDTGFYTLHV 124
QY 125 IKSDLVNEBATGQFRVYPELPEKPSISSNNNSKPYEDKDAVAFCEPEQDATYILMWVNS 184
DB 125 IKLNLMSERVGTQFVHPETPKPSISSNNNSPVEDKDAVAFCEPEQDATYILMWVNS 184
QY 185 LVPSPRLQSLNSGNRTLTLPNTTRNDTASYKCEQONPVARSDSYILNVLYGPDAP 244
DB 185 LVPSPRLQSLNSGNRTLTLPNTTRNDTASYKCEQONPVARSDSYILNVLYGPDAP 244
QY 245 LNTSYRSGENILNSCHASNPAPQYSWFVNGTFOOSTOELFIPNTTVNNSGSGYTCC 304
DB 245 SDTYHAGVNLNSCHASNPAPQYSWFVNGTFOOSTOELFIPNTTVNNSGSGYTCC 304
QY 305 DTGLNRTTYTITV 318
DB 305 DTGLNRTTYTITV 318
QY 305 ATGRRNRTTYRMITV 318
DB 305 ATGRRNRTTYRMITV 318
```

```
RESULT 14
5169835-2
; Patent No. 5169835
; APPLICANT: MAI-YEE, CHAN
; TITLE OF INVENTION: PREGNANCY SPECIFIC PROTEINS APPLICATIONS
; NUMBER OF SEQUENCES: 48
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/390,409
; FILING DATE: 07-AUG-1989
```

```
;SEQ ID NO:2:
; LENGTH: 419
5169835-2
```

```
Query Match 30.3%; Score 1126.5; DB 6; Length 419;
Best Local Similarity 46.9%; Pred. No. 1.6e-76;
Matches 234; Conservative 54; Mismatches 124; Indels 87; Gaps 3;
```

```
QY 1 MESPAAPPHRWCIPMORLLITASLITFMNPTTAKLTISTEPFNVAEGKVLVNLPHLFG 60
DB 1 MCTLSAPCTQRIKKGGLITASLITFMNPTTAKLTISTEPFNVAEGKVLVNLPHLFG 60
QY 61 HLFQSWYKGERVDGNROIGVIGTQATPGPAYSGREIIPNASLLIIONIDTGFY 120
DB 61 NLTYIWKQWRDLXHYITSYVVDGEIIPAYSGREIIPNASLLIIONIDTGFY 120
QY 121 TLHVTKSDLVNBEATGQ--FRVYPELPEKPSISSNNNSKPYEDKDAVAFCEPEQDATYIL 178
DB 121 TLHIIKGDGTRGVYGRFTLTLETPKPSISSNNNSPVEDKDAVAFCEPEQDATYIL 180
QY 179 WYNNQSLPVSPRLQSLNSGNRTLTLPNTTRNDTASYKCEQONPVARSDSYILNVLYGPD 238
DB 181 WYNNQSLPVSPRLQSLNSGNRTLTLPNTTRNDTASYKCEQONPVARSDSYILNVLYGPD 236
QY 239 APTISPLNTSYRSGENILNSCHASNPAPQYSWFVNGTFOOSTOELFIPNTTVNNSGSGYT 298
DB 237 -----PKL----- 239
QY 299 COAHNSDTGLNRTTYTITTYAAPPKPTITSNNNSPVEDKDAVAFCEPEQDATYILMWV 358
DB 240 -----PKYIITINNLPRENKQVNLNCEPKSENYIYWL 275
QY 359 NNQSLPVSPRLQSLNSGNRTLTLPNTTRNDTASYKCEQONPVARSDSYILNVLYGPD 418
DB 276 NNQSLPVSPRLQSLNSGNRTLTLPNTTRNDTASYKCEQONPVARSDSYILNVLYGPD 335
QY 419 TISPSYTYRRPQVNLNSCHASNPAPQYSWFVNGTFOOSTOELFIPNTTVNNSGSGYT 478
DB 336 RYPSFTYRSGEVLVYLSGADSNPAPQYSWFVNGTFOOSTOELFIPNTTVNNSGSGYT 395
QY 479 AANSGHSRTTYTITV 497
DB 396 VANSATGKSSKSMTEVVS 414
```

```
RESULT 15
5169835-6
; Patent No. 5169835
; APPLICANT: MAI-YEE, CHAN
; TITLE OF INVENTION: PREGNANCY SPECIFIC PROTEINS APPLICATIONS
; NUMBER OF SEQUENCES: 48
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/390,409
; FILING DATE: 07-AUG-1989
; SEQ ID NO:6:
; LENGTH: 424
5169835-6
```

```
Query Match 29.5%; Score 1099; DB 6; Length 424;
Best Local Similarity 46.9%; Pred. No. 1.9e-74;
Matches 232; Conservative 48; Mismatches 127; Indels 88; Gaps 4;
```

```
QY 5 SAPPHRWCIPMORLLITASLITFMNPTTAKLTISTEPFNVAEGKVLVNLPHLFG 64
DB 5 SAPCTQITWKGLITASLITFMNPTTAKLTISTEPFNVAEGKVLVNLPHLFG 64
QY 65 YSMYGERVDGNROIGVIGTQATPGPAYSGREIIPNASLLIIONIDTGFYTLHV 124
DB 65 YMYKGETVDANRIIGVYISNOQITPGPAYSGREIIPNASLLIIONIDTGFYTLHV 123
QY 125 IKSDLVNEBATGQFRV--YPELPEKPSISSNNNSKPYEDKDAVAFCEPEQDATYILMWV 182
DB 124 IKRGDTGVTGYFTVTLVSETPKPSISSNNNSPVEDKDAVAFCEPEQDATYILMWV 183
```


IS PAGE LEFT BLANK

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 10, 2006, 18:07:01 ; Search time 15.2574 Seconds

(without alignments)
1121.675 Million cell updates/sec

Title: US-10-734-564-100

Perfect score: 1124
Sequence: 1 MAPREPLASGILLMLIAP.....ACLPREPLCTWQSLRSGIA 207

Scoring table:

BIOSUN62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: Issued Patents_AA:*
2: /cgn2_6/ptodata/1/1aa/5_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/RTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1124	100.0	207	1	US-08-588-163-5 Sequence 5, Appl1
2	1124	100.0	207	1	US-09-111-070-5 Sequence 5, Appl1
3	1124	100.0	207	2	US-08-849-764C-5 Sequence 5, Appl1
4	1124	100.0	207	2	US-09-262-087-5 Sequence 5, Appl1
5	1124	100.0	207	2	US-08-463-261B-11 Sequence 11, Appl1
6	1124	100.0	207	2	US-09-540-530-1 Sequence 1, Appl1
7	1124	100.0	207	2	US-08-134-231C-23 Sequence 23, Appl1
8	1124	100.0	207	2	US-08-728-160-23 Sequence 23, Appl1
9	1124	100.0	207	2	US-10-116-064-5 Sequence 5, Appl1
10	1124	100.0	254	2	US-09-949-016-9699 Sequence 9699, Ap
11	1009	89.8	184	2	US-09-452-817-1 Sequence 1, Appl1
12	995	88.5	207	2	US-08-134-231C-22 Sequence 22, Appl1
13	995	88.5	207	2	US-08-728-160-22 Sequence 22, Appl1
14	902.5	80.3	206	2	US-08-134-231C-24 Sequence 24, Appl1
15	902.5	80.3	206	2	US-08-728-160-24 Sequence 24, Appl1
16	837.5	74.5	205	2	US-08-134-231C-25 Sequence 25, Appl1
17	837.5	74.5	205	2	US-08-728-160-25 Sequence 25, Appl1
18	579	51.5	106	2	US-09-452-817-2 Sequence 2, Appl1
19	415.5	37.0	220	1	US-08-588-163-3 Sequence 3, Appl1
20	415.5	37.0	220	1	US-09-111-070-3 Sequence 3, Appl1
21	415.5	37.0	220	2	US-09-540-530-2 Sequence 2, Appl1
22	415.5	37.0	220	2	US-08-134-231C-27 Sequence 27, Appl1
23	415.5	37.0	220	2	US-09-660-107-11 Sequence 11, Appl1
24	415.5	37.0	220	2	US-08-728-160-27 Sequence 27, Appl1
25	415.5	37.0	220	2	US-08-803-954B-9 Sequence 9, Appl1
26	407.5	36.3	218	2	US-08-849-764C-3 Sequence 3, Appl1
27	407.5	36.3	218	2	US-09-262-087-3 Sequence 3, Appl1

28	407.5	36.3	218	2	US-08-463-261B-9 Sequence 9, Appl1
29	407.5	36.3	218	2	US-10-116-064-3 Sequence 3, Appl1
30	394.5	35.1	220	2	US-08-134-231C-26 Sequence 26, Appl1
31	394.5	35.1	220	2	US-08-728-160-26 Sequence 26, Appl1
32	394.5	35.1	220	2	US-08-803-954B-7 Sequence 7, Appl1
33	389.5	34.7	211	1	US-08-588-163-4 Sequence 4, Appl1
34	389.5	34.7	211	1	US-09-111-070-4 Sequence 4, Appl1
35	389.5	34.7	211	2	US-09-540-530-3 Sequence 3, Appl1
36	389.5	34.7	211	2	US-08-134-231C-13 Sequence 13, Appl1
37	389.5	34.7	211	2	US-08-728-160-13 Sequence 13, Appl1
38	389.5	34.7	211	2	US-09-949-016-5932 Sequence 5932, Ap
39	389.5	34.7	212	2	US-09-949-016-10868 Sequence 10868, A
40	388.5	34.6	212	2	US-08-134-231C-29 Sequence 29, Appl1
41	388.5	34.6	212	2	US-08-728-160-29 Sequence 29, Appl1
42	384	34.2	210	2	US-08-849-764C-4 Sequence 4, Appl1
43	384	34.2	210	2	US-09-262-087-4 Sequence 4, Appl1
44	384	34.2	210	2	US-08-463-261B-10 Sequence 10, Appl1
45	384	34.2	210	2	US-10-116-064-4 Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-08-588-163-5
; Sequence 5, Application US/08588163
; Patent No. 5643752
; GENERAL INFORMATION:
; APPLICANT: Hawking, Phillip R.
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: A NOVEL TISSUE INHIBITOR OF
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESS: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/588,163
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J.
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: PF-0053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 207 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: METALLOPROTEINASES
; CLONE: TIME-1
; US-08-588-163-5
Query Match 100.0%; Score 1124; DB 1; Length 207;

Best Local Similarity 100.0%; Pred. No. 8.5e-128;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPFEPPLASGILLMLLMLIAPSRACCTVPPHPQTAFNSDLVIRAKVGTPEVNOGTLTYOR 60
DB 1 MAPFEPPLASGILLMLLMLIAPSRACCTVPPHPQTAFNSDLVIRAKVGTPEVNOGTLTYOR 60
QY 61 YEIKTKTKYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSSEFLIAGKLODGLLHTT 120
DB 61 YEIKTKTKYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSSEFLIAGKLODGLLHTT 120
QY 121 TCSFVAPMNSLSLAORRGFTKTYTGCECTVFPCLSIIPCKLOSGTHCLMTDQLLOGSEK 180
DB 121 TCSFVAPMNSLSLAORRGFTKTYTGCECTVFPCLSIIPCKLOSGTHCLMTDQLLOGSEK 180
QY 181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
DB 181 GFQSRHLACLPREPGLCTWQSLRSQIA 207

RESULT 2

US-09-111-070-5
; Sequence 5, Application US/09111070
; Patent No. 5914392

GENERAL INFORMATION:

APPLICANT: Hawkins, Phillip R.

TITLE OF INVENTION: A NOVEL TISSUE INHIBITOR OF

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: US

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: IBM Compatible

SOFTWARE: FASTSEQ Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/111,070

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/588,163

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Luther, Barbara J.

REGISTRATION NUMBER: 33,954

REFERENCE/DOCKET NUMBER: PF-0053

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEFAX: 415-852-0195

TELEX:

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 207 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

IMMEDIATE SOURCE:

LIBRARY: METALLOPROTEINASES

CLONE: TIMP-1

US-09-111-070-5

Query Match 100.0%; Score 1124; DB 1; Length 207;
Best Local Similarity 100.0%; Pred. No. 8.5e-128;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPFEPPLASGILLMLLMLIAPSRACCTVPPHPQTAFNSDLVIRAKVGTPEVNOGTLTYOR 60
DB 1 MAPFEPPLASGILLMLLMLIAPSRACCTVPPHPQTAFNSDLVIRAKVGTPEVNOGTLTYOR 60
QY 61 YEIKTKTKYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSSEFLIAGKLODGLLHTT 120
DB 61 YEIKTKTKYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSSEFLIAGKLODGLLHTT 120
QY 121 TCSFVAPMNSLSLAORRGFTKTYTGCECTVFPCLSIIPCKLOSGTHCLMTDQLLOGSEK 180
DB 121 TCSFVAPMNSLSLAORRGFTKTYTGCECTVFPCLSIIPCKLOSGTHCLMTDQLLOGSEK 180
QY 181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
DB 181 GFQSRHLACLPREPGLCTWQSLRSQIA 207

RESULT 3

US-08-849-764C-5
; Sequence 5, Application US/08849764C
; Patent No. 6300310

GENERAL INFORMATION:

APPLICANT: GREENE, JOHN M

ROSEN, CRAIG

TITLE OF INVENTION: HUMAN TISSUE INHIBITOR OF

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: HUMAN GENOME SCIENCES, INC.

STREET: 9410 KEY WEST AVENUE

CITY: ROCKVILLE

STATE: MD

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/849,764C

FILING DATE: 19-Sep-1997

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: MICHELE M. WALES

REGISTRATION NUMBER: 43,975

REFERENCE/DOCKET NUMBER: PF148US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 301-309-8504

TELEFAX: 301-309-8439

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 207 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-08-849-764C-5

Query Match

Best Local Similarity 100.0%; Score 1124; DB 2; Length 207;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPFEPPLASGILLMLLMLIAPSRACCTVPPHPQTAFNSDLVIRAKVGTPEVNOGTLTYOR 60
DB 1 MAPFEPPLASGILLMLLMLIAPSRACCTVPPHPQTAFNSDLVIRAKVGTPEVNOGTLTYOR 60
QY 61 YEIKTKTKYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSSEFLIAGKLODGLLHTT 120
DB 61 YEIKTKTKYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSSEFLIAGKLODGLLHTT 120
QY 121 TCSFVAPMNSLSLAORRGFTKTYTGCECTVFPCLSIIPCKLOSGTHCLMTDQLLOGSEK 180
DB 121 TCSFVAPMNSLSLAORRGFTKTYTGCECTVFPCLSIIPCKLOSGTHCLMTDQLLOGSEK 180

Db 121 TCSTFVAPWNSLSLAQRGFTKTYTGCECTVFPCLSI PCKLQSGTHCLMTDQLQSGSEK 180
QY 181 GFOSRHILACLPRBPGLCTWQSLRSQIA 207
Db 181 GFOSRHILACLPRBPGLCTWQSLRSQIA 207

RESULT 4
US-09-262-087-5
; Sequence 5, Application US/09262087
; Patent No. 6391853
; GENERAL INFORMATION:
; APPLICANT: GREENE, JOHN M
; APPLICANT: ROSEN, CRAIG
; TITLE OF INVENTION: HUMAN TISSUE INHIBITOR OF
; TITLE OF INVENTION: METALLOPROTEINASE-4
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/262,087
; FILING DATE: 04-MAR-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/463,261
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/14498
; FILING DATE: 13-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: A. ANDERS BROOKES
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PFI48P1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 207 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-262-087-5

Query Match 100.0%; Score 1124; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 8.5e-128;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPEPLASGILLMLIAPSRACVPPHQTAFCSNDLVIRAKFVGTPEVNOCTTLXOR 60
Db 1 MAPEPLASGILLMLIAPSRACVPPHQTAFCSNDLVIRAKFVGTPEVNOCTTLXOR 60
QY 61 YEIMTKYKGFQALGDAADIRFYVTPAMESVCGYFHRSHNRSEFFLIAGKLQDGLHIT 120
Db 61 YEIMTKYKGFQALGDAADIRFYVTPAMESVCGYFHRSHNRSEFFLIAGKLQDGLHIT 120
QY 121 TCSTFVAPWNSLSLAQRGFTKTYTGCECTVFPCLSI PCKLQSGTHCLMTDQLQSGSEK 180
Db 121 TCSTFVAPWNSLSLAQRGFTKTYTGCECTVFPCLSI PCKLQSGTHCLMTDQLQSGSEK 180
QY 181 GFOSRHILACLPRBPGLCTWQSLRSQIA 207

Db 181 GFOSRHILACLPRBPGLCTWQSLRSQIA 207

RESULT 5
US-08-463-261B-11
; Sequence 11, Application US/08463261B
; Patent No. 6448042
; GENERAL INFORMATION:
; APPLICANT: John M. Greene and Craig A. Rosen
; TITLE OF INVENTION: Human Tissue Inhibitor of Metalloproteinase-4
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,261B
; FILING DATE: 05-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/14498
; FILING DATE: 13-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: KENLEY K. HOOVER
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PFI48P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-610-5790
; TELEFAX: 301-610-8439
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 207 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; US-08-463-261B-11

Query Match 100.0%; Score 1124; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 8.5e-128;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPEPLASGILLMLIAPSRACVPPHQTAFCSNDLVIRAKFVGTPEVNOCTTLXOR 60
Db 1 MAPEPLASGILLMLIAPSRACVPPHQTAFCSNDLVIRAKFVGTPEVNOCTTLXOR 60
QY 61 YEIMTKYKGFQALGDAADIRFYVTPAMESVCGYFHRSHNRSEFFLIAGKLQDGLHIT 120
Db 61 YEIMTKYKGFQALGDAADIRFYVTPAMESVCGYFHRSHNRSEFFLIAGKLQDGLHIT 120
QY 121 TCSTFVAPWNSLSLAQRGFTKTYTGCECTVFPCLSI PCKLQSGTHCLMTDQLQSGSEK 180
Db 121 TCSTFVAPWNSLSLAQRGFTKTYTGCECTVFPCLSI PCKLQSGTHCLMTDQLQSGSEK 180
QY 181 GFOSRHILACLPRBPGLCTWQSLRSQIA 207

RESULT 6
US-09-540-530-1
; Sequence 1, Application US/09540530
; Patent No. 6534635
; GENERAL INFORMATION:

APPLICANT: Miyazaki, Kaoru
APPLICANT: Higashi, Shouichi
TITLE OF INVENTION: MODIFIED TIMP
FILE REFERENCE: 159-57
CURRENT APPLICATION NUMBER: US/09/540,530
CURRENT FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: JP 95142/1999
PRIOR FILING DATE: 1999-04-01
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 207
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: modified TIMP
US-09-540-530-1

Query Match 100.0%; Score 1124; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 8.5e-128;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPPEPLASGILLMLLAPSRACVCPHPQTAFCNSDLVIRAKFVGTPENVQTTLYOR 60
DB 1 MAPPEPLASGILLMLLAPSRACVCPHPQTAFCNSDLVIRAKFVGTPENVQTTLYOR 60
QY 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSSEFLIAGKLODGLLHT 120
DB 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSSEFLIAGKLODGLLHT 120
QY 121 TCSFVAPMNSLSLAQRGFTKTYTGCECTVFPCLSIIPCKLOSGTHCLMTDQLQSGSEK 180
DB 121 TCSFVAPMNSLSLAQRGFTKTYTGCECTVFPCLSIIPCKLOSGTHCLMTDQLQSGSEK 180
QY 181 GFQSRHLACLPREPGICTWQSLRSQIA 207
DB 181 GFQSRHLACLPREPGICTWQSLRSQIA 207

RESULT 7
US-08-134-231C-23
Sequence 23, Application US/08134231C
Patent No. 6562596
GENERAL INFORMATION:
APPLICANT: Koshi, Raymond A.
TITLE OF INVENTION: Tissue Inhibitor Metalloproteinase Type
Three (TIMP-3) Composition and Methods
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSER: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/134,231C
FILING DATE: 06-Oct-1993
CLASSIFICATION: <Unknown>
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 207 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 23:

US-08-134-231C-23

Query Match 100.0%; Score 1124; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 8.5e-128;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPPEPLASGILLMLLAPSRACVCPHPQTAFCNSDLVIRAKFVGTPENVQTTLYOR 60
DB 1 MAPPEPLASGILLMLLAPSRACVCPHPQTAFCNSDLVIRAKFVGTPENVQTTLYOR 60
QY 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSSEFLIAGKLODGLLHT 120
DB 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSSEFLIAGKLODGLLHT 120
QY 121 TCSFVAPMNSLSLAQRGFTKTYTGCECTVFPCLSIIPCKLOSGTHCLMTDQLQSGSEK 180
DB 121 TCSFVAPMNSLSLAQRGFTKTYTGCECTVFPCLSIIPCKLOSGTHCLMTDQLQSGSEK 180
QY 181 GFQSRHLACLPREPGICTWQSLRSQIA 207
DB 181 GFQSRHLACLPREPGICTWQSLRSQIA 207

RESULT 8
US-08-728-160-23
Sequence 23, Application US/08728160
Patent No. 6683155
GENERAL INFORMATION:
APPLICANT: Koshi, Raymond A.
TITLE OF INVENTION: Tissue Inhibitor Metalloproteinase Type
Three (TIMP-3) Composition and Methods
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSER: Amgen Inc./Patent Operations/KMP
STREET: 1840 Dehaven Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,160
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/134,231
FILING DATE:
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 207 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-728-160-23

Query Match 100.0%; Score 1124; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 8.5e-128;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPPEPLASGILLMLLAPSRACVCPHPQTAFCNSDLVIRAKFVGTPENVQTTLYOR 60
DB 1 MAPPEPLASGILLMLLAPSRACVCPHPQTAFCNSDLVIRAKFVGTPENVQTTLYOR 60
QY 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSSEFLIAGKLODGLLHT 120
DB 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSSEFLIAGKLODGLLHT 120

QY 121 TCSFVAPMNSLSLAORRGFTKTYTGCEBCTVFPCLSIIPCKLOSGTHCLMTDOLLQSEK 180
DB 121 TCSFVAPMNSLSLAORRGFTKTYTGCEBCTVFPCLSIIPCKLOSGTHCLMTDOLLQSEK 180
QY 181 GFOSRHIACLPREPGLCTWOSLRQIA 207
DB 181 GFOSRHIACLPREPGLCTWOSLRQIA 207

RESULT 9

US-10-116-064-5
Sequence 5, Application US/10116064
Patent No. 6828424
GENERAL INFORMATION:
APPLICANT: GREENE, JOHN M
ROSEN, CRAIG
TITLE OF INVENTION: HUMAN TISSUE INHIBITOR OF
METALLOPROTEINASE-4
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESS: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVE
CITY: ROCKVILLE
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/116,064
FILING DATE: 05-APR-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/262,087
FILING DATE: 04-MAR-1999
APPLICATION NUMBER: PCT/US94/14498
FILING DATE: 13-FEB-1994
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 207 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-116-064-5

Query Match 100.0%; Score 1124; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 8.5e-128;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPEPLASGILLMLTIAPSRACVPPHPQTAFCNSDLVIRAKFVGPTEVNOGTTLYOR 60
DB 1 MAPEPLASGILLMLTIAPSRACVPPHPQTAFCNSDLVIRAKFVGPTEVNOGTTLYOR 60
QY 61 YEIMTKMYKGFQALGDAADIRFYVTPAMESVCGYFHRSHNRSEFLIAGLQDGLHIT 120
DB 61 YEIMTKMYKGFQALGDAADIRFYVTPAMESVCGYFHRSHNRSEFLIAGLQDGLHIT 120
QY 121 TCSFVAPMNSLSLAORRGFTKTYTGCEBCTVFPCLSIIPCKLOSGTHCLMTDOLLQSEK 180
DB 121 TCSFVAPMNSLSLAORRGFTKTYTGCEBCTVFPCLSIIPCKLOSGTHCLMTDOLLQSEK 180
QY 181 GFOSRHIACLPREPGLCTWOSLRQIA 207
DB 181 GFOSRHIACLPREPGLCTWOSLRQIA 207

RESULT 10
US-09-949-016-9699

Sequence 9699, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001107
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9699
LENGTH: 254
TYPE: PRT
ORGANISM: Human
US-09-949-016-9699

Query Match 100.0%; Score 1124; DB 2; Length 254;
Best Local Similarity 100.0%; Pred. No. 1.2e-127;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPEPLASGILLMLTIAPSRACVPPHPQTAFCNSDLVIRAKFVGPTEVNOGTTLYOR 60
DB 48 MAPEPLASGILLMLTIAPSRACVPPHPQTAFCNSDLVIRAKFVGPTEVNOGTTLYOR 107
QY 61 YEIMTKMYKGFQALGDAADIRFYVTPAMESVCGYFHRSHNRSEFLIAGLQDGLHIT 120
DB 108 YEIMTKMYKGFQALGDAADIRFYVTPAMESVCGYFHRSHNRSEFLIAGLQDGLHIT 167
QY 121 TCSFVAPMNSLSLAORRGFTKTYTGCEBCTVFPCLSIIPCKLOSGTHCLMTDOLLQSEK 180
DB 168 TCSFVAPMNSLSLAORRGFTKTYTGCEBCTVFPCLSIIPCKLOSGTHCLMTDOLLQSEK 227
QY 181 GFOSRHIACLPREPGLCTWOSLRQIA 207
DB 228 GFOSRHIACLPREPGLCTWOSLRQIA 254

RESULT 11
US-09-452-817-1
Sequence 1, Application US/09452817
Patent No. 6342374
GENERAL INFORMATION:
APPLICANT: Carmichael, David F
ANDERSON, David C
APPLICANT: Stricklin, George P
APPLICANT: Welgus, Howard G
TITLE OF INVENTION: Human Collagenase Inhibitor; Recombinant Vector System
TITLE OF INVENTION: For Using Same And Recombinant-DNA Method For
FILE REFERENCE: Serial No. 6342374 09/452,817
CURRENT APPLICATION NUMBER: US/09/452,817
CURRENT FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 08/474,553
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/050,739
PRIOR FILING DATE: 1993-04-21
PRIOR APPLICATION NUMBER: 07/853,018
PRIOR FILING DATE: 1992-03-18
PRIOR APPLICATION NUMBER: 07/517,475
PRIOR FILING DATE: 1990-05-01
PRIOR APPLICATION NUMBER: 07/320,923
PRIOR FILING DATE: 1989-03-08
PRIOR APPLICATION NUMBER: 06/784,319
PRIOR FILING DATE: 1985-10-04
PRIOR APPLICATION NUMBER: 06/699,181
PRIOR FILING DATE: 1985-02-05

NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO: 1
LENGTH: 184
TYPE: PRT
ORGANISM: Homo sapiens
US-09-452-817-1

Query Match
Best Local Similarity 100.0%; Score 1009; DB 2; Length 184;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 CTCVPHPTAFCSNDLVIRAKFVGTPEVNOQTLVYREIKMTKMYKGFQALGDAADIRF 83
DB 1 CTCVPHPTAFCSNDLVIRAKFVGTPEVNOQTLVYREIKMTKMYKGFQALGDAADIRF 60
QY 84 VYTPAMESVCGYFHRSHNSSEFLNGKLODGLHITTSFVAPMNSLSLAQRGGTKTY 143
DB 61 VYTPAMESVCGYFHRSHNSSEFLNGKLODGLHITTSFVAPMNSLSLAQRGGTKTY 120
QY 144 TVGCECTVFPCLSTPCKLOSGTHCLMTDQLQSGSEKGFOSRHILACLPREPGLCTWQSDR 203
DB 121 TVGCECTVFPCLSTPCKLOSGTHCLMTDQLQSGSEKGFOSRHILACLPREPGLCTWQSDR 180
QY 204 SQIA 207
DB 181 SQIA 184

RESULT 12

US-08-134-231C-22
Sequence 22, Application US/08134231C
Patent No. 6562596
GENERAL INFORMATION:
APPLICANT: Slibiger, Scott M.
Koski, Raymond A.
TITLE OF INVENTION: Tissue Inhibitor Metalloproteinase Type
Three (TMP-3) Composition and Methods
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/134,231C
FILING DATE: 06-Oct-1993
CLASSIFICATION: <Unknown>
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 207 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-08-134-231C-22

Query Match
Best Local Similarity 88.5%; Score 995; DB 2; Length 207;
Matches 180; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

QY 1 MAPFEPLASGILLMLLAPSRACCTVPPHPTAFCSNDLVIRAKFVGTPEVNOQTLVYR 60
DB 1 MAPFAPMASGILLMLLAPSRACCTVPPHPTAFCSNDLVIRAKFVGTAEVNETALVYR 60

QY 61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNSSEFLNGKLODGLHIT 120
DB 61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNSSEFLNGKLODGLHIT 120
QY 121 TCSFVAPMNSLSLAQRGGTKTYTVGCECTVFPCLSTPCKLOSGTHCLMTDQLQSGSEK 180
DB 121 TCSFVAPMNSLSLAQRGGTKTYTVGCECTVFPCLSTPCKLOSGTHCLMTDQLQSGSEK 180
QY 181 GFOSRHILACLPREPGLCTWQSDR 207
DB 181 GFOSRHILACLPREPGLCTWQSDR 207

RESULT 13

US-08-728-160-22
Sequence 22, Application US/08728160
Patent No. 6683155
GENERAL INFORMATION:
APPLICANT: Slibiger, Scott M.
Koski, Raymond A.
TITLE OF INVENTION: Tissue Inhibitor Metalloproteinase Type
Three (TMP-3) Composition and Methods
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc./Patent Operations/TMP
STREET: 1840 Dehaven Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,160
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/134,231
FILING DATE:
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 207 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-728-160-22

Query Match
Best Local Similarity 88.5%; Score 995; DB 2; Length 207;
Matches 180; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

QY 1 MAPFEPLASGILLMLLAPSRACCTVPPHPTAFCSNDLVIRAKFVGTPEVNOQTLVYR 60
DB 1 MAPFAPMASGILLMLLAPSRACCTVPPHPTAFCSNDLVIRAKFVGTAEVNETALVYR 60
QY 61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNSSEFLNGKLODGLHIT 120
DB 61 YEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNSSEFLNGKLODGLHIT 120
QY 121 TCSFVAPMNSLSLAQRGGTKTYTVGCECTVFPCLSTPCKLOSGTHCLMTDQLQSGSEK 180
DB 121 TCSFVAPMNSLSLAQRGGTKTYTVGCECTVFPCLSTPCKLOSGTHCLMTDQLQSGSEK 180
QY 181 GFOSRHILACLPREPGLCTWQSDR 207
DB 181 GFOSRHILACLPREPGLCTWQSDR 207

RESULT 14

US-08-134-231C-24
Sequence 24, Application US/08134231C
Patent No. 6562596
GENERAL INFORMATION:
APPLICANT: Silbiger, Scott M.
Koski, Raymond A.
TITLE OF INVENTION: Tissue Inhibitor Metalloproteinase Type
Three (TIMP-3) Composition and Methods
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/134,231C
FILING DATE: 06-Oct-1993
CLASSIFICATION: <Unknown>
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 206 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-08-134-231C-24
Query Match 80.3%; Score 902.5; DB 2; Length 206;
Best Local Similarity 80.8%; Pred. No. 6e-101;
Matches 164; Conservative 13; Mismatches 25; Indels 1; Gaps 1;
QY 1 MAPEPLASGILLMLIAPSRACVPPHPQTAFCNSDLVIRAKFVGTPEVNOTTLVOR 60
DB 1 MAPLAALASSMLLMLIAPSRACVPPHPQTAFCNSDLVIRAKFVGAPEVNHNTTLVOR 60
QY 61 YEIKMTKMGKGFQALGDADIRFYVTPAMESVCGYFHRSHNRSEBFLIAGLQDGLHIT 120
DB 61 YEIKMTKMGKGFQALGDADIRFYVTPAMESVCGYFHRSHNRSEBFLIAGLQDGLHIT 120
QY 121 TCSFVAPWNSLSLAQRGFTKTYTVGCECTVPCLSIIPCKLQSGTHCLMTDOLQSEK 180
DB 121 TCSFVAPWNSLSFSQSGFTKTYTVAGCDMCTVFACASIPCHLBSDTHTCLMTDSSL-GSDK 179
QY 181 GFQSRHLACLPRPGLCTWQSLR 203
DB 180 GFQSRHLACLPRPGLCTWQSLR 202
RESULT 15
US-08-728-160-24
Sequence 24, Application US/08728160
Patent No. 6683155
GENERAL INFORMATION:
APPLICANT: Silbiger, Scott M.
Koski, Raymond A.
TITLE OF INVENTION: Tissue Inhibitor Metalloproteinase Type
Three (TIMP-3) Composition and Methods
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc./Patent Operations/KMP
STREET: 1640 Denavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,160
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/134,231
FILING DATE:
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 206 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-728-160-24

Query Match 80.3%; Score 902.5; DB 2; Length 206;
Best Local Similarity 80.8%; Pred. No. 6e-101;
Matches 164; Conservative 13; Mismatches 25; Indels 1; Gaps 1;
QY 1 MAPEPLASGILLMLIAPSRACVPPHPQTAFCNSDLVIRAKFVGTPEVNOTTLVOR 60
DB 1 MAPLAALASSMLLMLIAPSRACVPPHPQTAFCNSDLVIRAKFVGAPEVNHNTTLVOR 60
QY 61 YEIKMTKMGKGFQALGDADIRFYVTPAMESVCGYFHRSHNRSEBFLIAGLQDGLHIT 120
DB 61 YEIKMTKMGKGFQALGDADIRFYVTPAMESVCGYFHRSHNRSEBFLIAGLQDGLHIT 120
QY 121 TCSFVAPWNSLSLAQRGFTKTYTVGCECTVPCLSIIPCKLQSGTHCLMTDOLQSEK 180
DB 121 TCSFVAPWNSLSFSQSGFTKTYTVAGCDMCTVFACASIPCHLBSDTHTCLMTDSSL-GSDK 179
QY 181 GFQSRHLACLPRPGLCTWQSLR 203
DB 180 GFQSRHLACLPRPGLCTWQSLR 202

Search completed: April 10, 2006, 18:08:44
Job time : 16.2574 secs

THIS PAGE LEFT BLANK

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: April 10, 2006, 18:07:51 ; Search time 53.0594 Seconds
(without alignments)
1630.072 Million cell updates/sec

Title: US-10-734-564-100

Perfect score: 1124
Sequence: 1 MAPPEPLASGILLMLIAP.....ACLRREPGLCTWQSLRSQIA 207

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1124	100.0	207	4	US-10-116-064-5
2	1124	100.0	207	4	US-10-348-167-23
3	1124	100.0	207	4	US-10-301-882-205
4	1124	100.0	207	4	US-10-087-188-4
5	1124	100.0	207	4	US-10-325-446-1
6	1124	100.0	207	4	US-10-712-124-70
7	1124	100.0	207	4	US-10-734-564-100
8	1124	100.0	207	5	US-10-486-090-9
9	1124	100.0	207	5	US-10-971-461-20
10	1124	100.0	207	5	US-10-852-335A-129
11	1124	100.0	207	5	US-10-971-195-4
12	1124	100.0	207	6	US-11-037-713-52
13	1120	99.6	207	6	US-09-731-872-291
14	1120	99.6	207	3	US-09-876-997-291
15	1120	99.6	207	5	US-10-643-836-291
16	1034	92.0	204	4	US-10-264-049-338
17	1010	89.9	580	4	US-10-025-514-18
18	1010	89.9	580	6	US-11-077-276-18
19	1009	89.8	184	4	US-10-025-514-6
20	1009	89.8	184	6	US-11-077-276-6
21	1009	89.8	580	6	US-10-025-514-10
22	1009	89.8	580	6	US-11-077-276-10
23	995	88.5	207	4	US-10-348-167-22
24	902.5	80.3	206	4	US-10-348-167-24
25	895	79.6	166	4	US-10-372-683-6
26	837.5	74.5	205	4	US-10-348-167-25
27	782.5	69.6	183	3	US-09-925-301-1594

28	728.5	64.8	212	4	US-10-264-049-3513	Sequence 3513, App
29	715	63.6	162	4	US-10-264-049-3566	Sequence 3566, App
30	691	61.5	128	6	US-10-025-514-24	Sequence 24, Appl
31	691	61.5	128	6	US-11-077-276-24	Sequence 24, Appl
32	683	60.8	522	4	US-10-025-514-20	Sequence 20, Appl
33	683	60.8	522	6	US-11-077-276-20	Sequence 20, Appl
34	682	60.7	127	4	US-10-025-514-32	Sequence 22, Appl
35	682	60.7	127	6	US-11-077-276-22	Sequence 22, Appl
36	682	60.7	522	4	US-10-025-514-14	Sequence 14, Appl
37	682	60.7	522	6	US-11-077-276-14	Sequence 14, Appl
38	587.5	52.3	136	6	US-11-097-369-2	Sequence 2, Appl
39	485	43.1	92	4	US-10-425-115-202109	Sequence 202109, Appl
40	415.5	37.0	220	4	US-10-348-167-32	Sequence 27, Appl
41	415.5	37.0	220	4	US-10-325-446-2	Sequence 2, Appl
42	415.5	37.0	220	5	US-10-804-937A-7	Sequence 7, Appl
43	415.5	37.0	220	5	US-10-486-090-10	Sequence 10, Appl
44	415.5	37.0	220	5	US-10-971-461-21	Sequence 21, Appl
45	415.5	37.0	220	5	US-10-893-323-9	Sequence 9, Appl

ALIGNMENTS

```
RESULT 1
US-10-116-064-5
; Sequence 5, Application US/10116064
; Publication No. US20020115187A1
; GENERAL INFORMATION:
; APPLICANT: GREENE, JOHN M
; ROSEN, CRAIG
; TITLE OF INVENTION: HUMAN TISSUE INHIBITOR OF
; METALLOPROTEINASE-4
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/116,064
; FILING DATE: 05-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/262,087
; FILING DATE: 04-MAR-1999
; APPLICATION NUMBER: PCT/US94/14498
; FILING DATE: 13-FEB-1994
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 207 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-116-064-5
Query Match 100.0%; Score 1124; DB 4; Length 207;
Best Local Similarity 100.0%; Pred. No. 1.1e-111;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPPEPLASGILLMLIAPSRACVPPHPQTAFCNSDIVIRAKFYGTPEVNOQTLYOR 60
Db 1 MAPPEPLASGILLMLIAPSRACVPPHPQTAFCNSDIVIRAKFYGTPEVNOQTLYOR 60
QY 61 YEIMTMYGFGALGDAADIRFYTPAMSVGCFYRSHNRSEFLIACKLDGGLHIT 120
```

Db 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSEEFFLAGKLQDGLLHIT 120
QY 121 TCSFVAPMNSLSIAQRRGFTKTYTGCECTVFPCLISIPCKLOSQTHCLMTDQLQGSBK 180
Db 121 TCSFVAPMNSLSIAQRRGFTKTYTGCECTVFPCLISIPCKLOSQTHCLMTDQLQGSBK 180
QY 181 GFQSRHLACLPRPGLCTWQSLRSQIA 207
Db 181 GFQSRHLACLPRPGLCTWQSLRSQIA 207

RESULT 2
US-10-348-167-23
; Sequence 23, Application US/10348167
; Publication No. US20030143693A1
; GENERAL INFORMATION:
; APPLICANT: Silbiger, Scott M.
; Koekl, Raymond A.
; TITLE OF INVENTION: Tissue Inhibitor Metalloproteinase Type
; Three (TIME-3) Composition and Methods
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/348,167
; FILING DATE: 22-Jan-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/134,231
; FILING DATE: October 6, 1993
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 207 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-348-167-23

Query Match 100.0%; Score 1124; DB 4; Length 207;
Best Local Similarity 100.0%; Pred. No. 1,1e-111;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPFEPLASGILLMLIAPSRACVCPHPOTAFNCNSDLVIRAKFVGTPENVQTTLYOR 60
Db 1 MAPFEPLASGILLMLIAPSRACVCPHPOTAFNCNSDLVIRAKFVGTPENVQTTLYOR 60
QY 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSEEFFLAGKLQDGLLHIT 120
Db 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSEEFFLAGKLQDGLLHIT 120
QY 121 TCSFVAPMNSLSIAQRRGFTKTYTGCECTVFPCLISIPCKLOSQTHCLMTDQLQGSBK 180
Db 121 TCSFVAPMNSLSIAQRRGFTKTYTGCECTVFPCLISIPCKLOSQTHCLMTDQLQGSBK 180
QY 181 GFQSRHLACLPRPGLCTWQSLRSQIA 207
Db 181 GFQSRHLACLPRPGLCTWQSLRSQIA 207

RESULT 3

US-10-301-822-205
; Sequence 205, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamackar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MPW01-029P2RMM
; CURRENT APPLICATION NUMBER: US/10/301,822
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 205
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-301-822-205

Query Match 100.0%; Score 1124; DB 4; Length 207;
Best Local Similarity 100.0%; Pred. No. 1,1e-111;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPFEPLASGILLMLIAPSRACVCPHPOTAFNCNSDLVIRAKFVGTPENVQTTLYOR 60
Db 1 MAPFEPLASGILLMLIAPSRACVCPHPOTAFNCNSDLVIRAKFVGTPENVQTTLYOR 60
QY 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSEEFFLAGKLQDGLLHIT 120
Db 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSEEFFLAGKLQDGLLHIT 120
QY 121 TCSFVAPMNSLSIAQRRGFTKTYTGCECTVFPCLISIPCKLOSQTHCLMTDQLQGSBK 180
Db 121 TCSFVAPMNSLSIAQRRGFTKTYTGCECTVFPCLISIPCKLOSQTHCLMTDQLQGSBK 180
QY 181 GFQSRHLACLPRPGLCTWQSLRSQIA 207
Db 181 GFQSRHLACLPRPGLCTWQSLRSQIA 207

RESULT 4
US-10-087-188-4
; Sequence 4, Application US/10087188
; Publication No. US20030175686A1
; GENERAL INFORMATION:
; APPLICANT: Robe, Steven L.
; APPLICANT: Oh, Esther H.
; APPLICANT: Walsh, Michael
; TITLE OF INVENTION: Methods of Diagnosing Liver Fibrosis
; FILE REFERENCE: P-PW 4978
; CURRENT APPLICATION NUMBER: US/10/087,188
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 10/087,188
; PRIOR FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-087-188-4

Query Match 100.0%; Score 1124; DB 4; Length 207;
 Best Local Similarity 100.0%; Pred. No. 1.1e-11;
 Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPEPLASGILLMLIAPSRACVPPHQTAFCONSULVIRAKFVGTEPVNOGTLTYOR 60
 DB 1 MAPEPLASGILLMLIAPSRACVPPHQTAFCONSULVIRAKFVGTEPVNOGTLTYOR 60
 QY 61 YEIKMTKMYKGFQALGDAADIRFYVTPAMESVCGYFHRSHNRSEFFLIAGKLODGLHIT 120
 DB 61 YEIKMTKMYKGFQALGDAADIRFYVTPAMESVCGYFHRSHNRSEFFLIAGKLODGLHIT 120
 QY 121 TCSFVAPWNSLSLAQRGFTKTYTVGCECTVPCLSI PCKLOSGTHCLMTDOLLQSEK 180
 DB 121 TCSFVAPWNSLSLAQRGFTKTYTVGCECTVPCLSI PCKLOSGTHCLMTDOLLQSEK 180
 QY 181 GFOSRHILACLPREPGLCTWOSLRQIA 207
 DB 181 GFOSRHILACLPREPGLCTWOSLRQIA 207

RESULT 5

US-10-325-446-1
 ; Sequence 1, Application US/10325446
 ; Publication No. US20040121438A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Stephen Quirk
 ; TITLE OF INVENTION: Wound Care Compositions
 ; FILE REFERENCE: 1443.048US1
 ; CURRENT APPLICATION NUMBER: US/10/325,446
 ; CURRENT FILING DATE: 2002-12-19
 ; NUMBER OF SEQ ID NOS: 21
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 207
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-325-446-1

Query Match 100.0%; Score 1124; DB 4; Length 207;
 Best Local Similarity 100.0%; Pred. No. 1.1e-11;
 Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPEPLASGILLMLIAPSRACVPPHQTAFCONSULVIRAKFVGTEPVNOGTLTYOR 60
 DB 1 MAPEPLASGILLMLIAPSRACVPPHQTAFCONSULVIRAKFVGTEPVNOGTLTYOR 60
 QY 61 YEIKMTKMYKGFQALGDAADIRFYVTPAMESVCGYFHRSHNRSEFFLIAGKLODGLHIT 120
 DB 61 YEIKMTKMYKGFQALGDAADIRFYVTPAMESVCGYFHRSHNRSEFFLIAGKLODGLHIT 120
 QY 121 TCSFVAPWNSLSLAQRGFTKTYTVGCECTVPCLSI PCKLOSGTHCLMTDOLLQSEK 180
 DB 121 TCSFVAPWNSLSLAQRGFTKTYTVGCECTVPCLSI PCKLOSGTHCLMTDOLLQSEK 180
 QY 181 GFOSRHILACLPREPGLCTWOSLRQIA 207
 DB 181 GFOSRHILACLPREPGLCTWOSLRQIA 207

RESULT 6

US-10-712-124-70
 ; Sequence 70, Application US/10712124
 ; Publication No. US20040146907A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SMITH, VICTORIA
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING DYSPLASIA
 ; FILE REFERENCE: P2000R1
 ; CURRENT APPLICATION NUMBER: US/10/712,124
 ; CURRENT FILING DATE: 2003-11-13

PRIOR APPLICATION NUMBER: US 60/425,813
 ; PRIOR FILING DATE: 2002-11-13
 ; NUMBER OF SEQ ID NOS: 123
 ; SEQ ID NO 70
 ; LENGTH: 207
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 ; US-10-712-124-70

Query Match 100.0%; Score 1124; DB 4; Length 207;
 Best Local Similarity 100.0%; Pred. No. 1.1e-11;
 Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPEPLASGILLMLIAPSRACVPPHQTAFCONSULVIRAKFVGTEPVNOGTLTYOR 60
 DB 1 MAPEPLASGILLMLIAPSRACVPPHQTAFCONSULVIRAKFVGTEPVNOGTLTYOR 60
 QY 61 YEIKMTKMYKGFQALGDAADIRFYVTPAMESVCGYFHRSHNRSEFFLIAGKLODGLHIT 120
 DB 61 YEIKMTKMYKGFQALGDAADIRFYVTPAMESVCGYFHRSHNRSEFFLIAGKLODGLHIT 120
 QY 121 TCSFVAPWNSLSLAQRGFTKTYTVGCECTVPCLSI PCKLOSGTHCLMTDOLLQSEK 180
 DB 121 TCSFVAPWNSLSLAQRGFTKTYTVGCECTVPCLSI PCKLOSGTHCLMTDOLLQSEK 180
 QY 181 GFOSRHILACLPREPGLCTWOSLRQIA 207
 DB 181 GFOSRHILACLPREPGLCTWOSLRQIA 207

RESULT 7

US-10-734-564-100
 ; Sequence 100, Application US/10734564
 ; Publication No. US20040157278A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Christopher C Burgess et al
 ; TITLE OF INVENTION: Detection Methods Using TIMP1
 ; FILE REFERENCE: 1657/2012
 ; CURRENT APPLICATION NUMBER: US/10/734,564
 ; CURRENT FILING DATE: 2003-12-12
 ; NUMBER OF SEQ ID NOS: 138
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 100
 ; LENGTH: 207
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-734-564-100

Query Match 100.0%; Score 1124; DB 4; Length 207;
 Best Local Similarity 100.0%; Pred. No. 1.1e-11;
 Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPEPLASGILLMLIAPSRACVPPHQTAFCONSULVIRAKFVGTEPVNOGTLTYOR 60
 DB 1 MAPEPLASGILLMLIAPSRACVPPHQTAFCONSULVIRAKFVGTEPVNOGTLTYOR 60
 QY 61 YEIKMTKMYKGFQALGDAADIRFYVTPAMESVCGYFHRSHNRSEFFLIAGKLODGLHIT 120
 DB 61 YEIKMTKMYKGFQALGDAADIRFYVTPAMESVCGYFHRSHNRSEFFLIAGKLODGLHIT 120
 QY 121 TCSFVAPWNSLSLAQRGFTKTYTVGCECTVPCLSI PCKLOSGTHCLMTDOLLQSEK 180
 DB 121 TCSFVAPWNSLSLAQRGFTKTYTVGCECTVPCLSI PCKLOSGTHCLMTDOLLQSEK 180
 QY 181 GFOSRHILACLPREPGLCTWOSLRQIA 207
 DB 181 GFOSRHILACLPREPGLCTWOSLRQIA 207

RESULT 8

US-10-486-090-9
 ; Sequence 9, Application US/10486090
 ; Publication No. US20040235724A1

```
/ GENERAL INFORMATION:
/ APPLICANT: Berdel, Wolfgang E.
/ APPLICANT: Oelmann, Elisabeth
/ TITLE OF INVENTION: Use of TIMP-1 as an Immunosuppressant
/ FILE REFERENCE: 19235.002
/ CURRENT APPLICATION NUMBER: US/10/486,090
/ PRIOR FILING DATE: 2004-02-06
/ PRIOR APPLICATION NUMBER: PCT/EP02/08733
/ PRIOR FILING DATE: 2002-08-05
/ PRIOR APPLICATION NUMBER: DE 101 38 550.1
/ PRIOR FILING DATE: 2001-08-06
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: Patent in version 3.2
/ SEQ ID NO 9
/ LENGTH: 207
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic construct
US-10-486-090-9
```

```
Query Match      100.0%; Score 1124; DB 5; Length 207;
Best Local Similarity 100.0%; Pred. No. 1.1e-111;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 MAPFEPLASGILLMLLMLIAPSRACVPPHPOTAFNCNSDLVIRAKFVGTPENVQTTLYOR 60
DB      1 MAPFEPLASGILLMLLMLIAPSRACVPPHPOTAFNCNSDLVIRAKFVGTPENVQTTLYOR 60
QY      61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSSEFLIAGKLQDGLLHT 120
DB      61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSSEFLIAGKLQDGLLHT 120
QY      121 TCSFVAPMNSLSIAORRGFTKTYTGCECTVFPCLSTPCXKQSGTHCLMTDQLQGSSEK 180
DB      121 TCSFVAPMNSLSIAORRGFTKTYTGCECTVFPCLSTPCXKQSGTHCLMTDQLQGSSEK 180
QY      181 GFQSRHLACLPREPGLCTWQSIQSQA 207
DB      181 GFQSRHLACLPREPGLCTWQSIQSQA 207
```

```
RESULT 9
US-10-971-461-20
/ Sequence 20, Application US/10971461
/ Publication No. US20050070477A1
/ GENERAL INFORMATION:
/ APPLICANT: Cochrane, Charles G.
/ APPLICANT: The Scripps Research Institute
/ TITLE OF INVENTION: Treatment and Prevention of Pulmonary Conditions
/ FILE REFERENCE: 1361.037US1
/ CURRENT APPLICATION NUMBER: US/10/971,461
/ CURRENT FILING DATE: 2004-10-22
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: FaastSeq for windows Version 4.0
/ SEQ ID NO 20
/ LENGTH: 207
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-971-461-20
```

```
Query Match      100.0%; Score 1124; DB 5; Length 207;
Best Local Similarity 100.0%; Pred. No. 1.1e-111;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 MAPFEPLASGILLMLLMLIAPSRACVPPHPOTAFNCNSDLVIRAKFVGTPENVQTTLYOR 60
DB      1 MAPFEPLASGILLMLLMLIAPSRACVPPHPOTAFNCNSDLVIRAKFVGTPENVQTTLYOR 60
QY      61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSSEFLIAGKLQDGLLHT 120
DB      61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSSEFLIAGKLQDGLLHT 120
```

```
QY      121 TCSFVAPMNSLSIAORRGFTKTYTGCECTVFPCLSTPCXKQSGTHCLMTDQLQGSSEK 180
DB      121 TCSFVAPMNSLSIAORRGFTKTYTGCECTVFPCLSTPCXKQSGTHCLMTDQLQGSSEK 180
QY      181 GFQSRHLACLPREPGLCTWQSIQSQA 207
DB      181 GFQSRHLACLPREPGLCTWQSIQSQA 207
```

```
RESULT 10
US-10-852-335A-129
/ Sequence 129, Application US/10852335A
/ Publication No. US20050112129A1
/ GENERAL INFORMATION:
/ APPLICANT: HEIDI S. PHILLIPS
/ TITLE OF INVENTION: Compositions and Methods for the Diagnosis and
/ FILE REFERENCE: P5103RL-US
/ CURRENT APPLICATION NUMBER: US/10/852,335A
/ CURRENT FILING DATE: 2004-05-24
/ PRIOR APPLICATION NUMBER: US 60/548,299
/ PRIOR FILING DATE: 2004-02-27
/ PRIOR APPLICATION NUMBER: US 60/473,238
/ PRIOR FILING DATE: 2003-05-23
/ NUMBER OF SEQ ID NOS: 190
/ SEQ ID NO 129
/ LENGTH: 207
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-852-335A-129
```

```
Query Match      100.0%; Score 1124; DB 5; Length 207;
Best Local Similarity 100.0%; Pred. No. 1.1e-111;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 MAPFEPLASGILLMLLMLIAPSRACVPPHPOTAFNCNSDLVIRAKFVGTPENVQTTLYOR 60
DB      1 MAPFEPLASGILLMLLMLIAPSRACVPPHPOTAFNCNSDLVIRAKFVGTPENVQTTLYOR 60
QY      61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSSEFLIAGKLQDGLLHT 120
DB      61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSSEFLIAGKLQDGLLHT 120
QY      121 TCSFVAPMNSLSIAORRGFTKTYTGCECTVFPCLSTPCXKQSGTHCLMTDQLQGSSEK 180
DB      121 TCSFVAPMNSLSIAORRGFTKTYTGCECTVFPCLSTPCXKQSGTHCLMTDQLQGSSEK 180
QY      181 GFQSRHLACLPREPGLCTWQSIQSQA 207
DB      181 GFQSRHLACLPREPGLCTWQSIQSQA 207
```

```
RESULT 11
US-10-971-195-4
/ Sequence 4, Application US/10971195
/ Publication No. US20050186561A1
/ GENERAL INFORMATION:
/ APPLICANT: Oh, Esther H.
/ APPLICANT: Smith, Catherine M.
/ APPLICANT: Promethues Laboratories Inc.
/ TITLE OF INVENTION: Methods of Diagnosing Tissue Fibrosis
/ FILE REFERENCE: 021825-001310US
/ CURRENT APPLICATION NUMBER: US/10/971,195
/ CURRENT FILING DATE: 2004-10-22
/ PRIOR APPLICATION NUMBER: US 60/514,034
/ PRIOR FILING DATE: 2003-10-24
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: Patent in Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 207
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
```

```
QY      1 MAPFEPLASGILLMLLMLIAPSRACVPPHPOTAFNCNSDLVIRAKFVGTPENVQTTLYOR 60
DB      1 MAPFEPLASGILLMLLMLIAPSRACVPPHPOTAFNCNSDLVIRAKFVGTPENVQTTLYOR 60
QY      61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSSEFLIAGKLQDGLLHT 120
DB      61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSSEFLIAGKLQDGLLHT 120
```

OTHER INFORMATION: human tissue inhibitor of metalloproteinase-1
OTHER INFORMATION: (TIMP-1)
US-10-971-195-4

Query Match 100.0%; Score 1124; DB 5; Length 207;
Best Local Similarity 100.0%; Pred. No. 1,1e-111;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPEPLASGILLMLIAPSRACVCPHPQTAFCNSDLVIRAKFVGTPEVNOITLYOR 60
DB 1 MAPEPLASGILLMLIAPSRACVCPHPQTAFCNSDLVIRAKFVGTPEVNOITLYOR 60
QY 61 YEIMTKMYKGFQALGDAADIRFYVTPAMESVCGYFHRSHNRSEFLIAGKLODGLHIT 120
DB 61 YEIMTKMYKGFQALGDAADIRFYVTPAMESVCGYFHRSHNRSEFLIAGKLODGLHIT 120
QY 121 TCSFVAWPNWSLSLAQRGFTKTYVGCSECTVFPCLSIIPCKLOSGTHCLMTDOLLOSEK 180
DB 121 TCSFVAWPNWSLSLAQRGFTKTYVGCSECTVFPCLSIIPCKLOSGTHCLMTDOLLOSEK 180
QY 181 GFOSRHILACLPREPGLCTWOSLSRQIA 207
DB 181 GFOSRHILACLPREPGLCTWOSLSRQIA 207

RESULT 12

US-11-037-713-52
Sequence 52, Application US/11037713
Publication No. US20050221398A1
GENERAL INFORMATION:
APPLICANT: JACQUEMIER, JOCELYNE
APPLICANT: BERTUCCI, FRANCOIS
APPLICANT: BIRNBAUM, DANIEL
APPLICANT: DEBONO, STEPHANE
APPLICANT: TASETTI, REBECCA
TITLE OF INVENTION: PROTEIN EXPRESSION PROFILING AND BREAST CANCER
FILE REFERENCE: 1016-R-04 (B)
CURRENT APPLICATION NUMBER: US/11/037,713
PRIOR FILING DATE: 2005-01-18
PRIOR APPLICATION NUMBER: 60/537,412
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 52
LENGTH: 207
TYPE: PRT
ORGANISM: Homo sapiens
US-11-037-713-52

Query Match 100.0%; Score 1124; DB 6; Length 207;
Best Local Similarity 100.0%; Pred. No. 1,1e-111;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPEPLASGILLMLIAPSRACVCPHPQTAFCNSDLVIRAKFVGTPEVNOITLYOR 60
DB 1 MAPEPLASGILLMLIAPSRACVCPHPQTAFCNSDLVIRAKFVGTPEVNOITLYOR 60
QY 61 YEIMTKMYKGFQALGDAADIRFYVTPAMESVCGYFHRSHNRSEFLIAGKLODGLHIT 120
DB 61 YEIMTKMYKGFQALGDAADIRFYVTPAMESVCGYFHRSHNRSEFLIAGKLODGLHIT 120
QY 121 TCSFVAWPNWSLSLAQRGFTKTYVGCSECTVFPCLSIIPCKLOSGTHCLMTDOLLOSEK 180
DB 121 TCSFVAWPNWSLSLAQRGFTKTYVGCSECTVFPCLSIIPCKLOSGTHCLMTDOLLOSEK 180
QY 181 GFOSRHILACLPREPGLCTWOSLSRQIA 207
DB 181 GFOSRHILACLPREPGLCTWOSLSRQIA 207

RESULT 13
US-09-731-872-291

Sequence 291, Application US/09731872
Patent No. US20020102604A1

GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Bougueleret, Lydie
APPLICANT: Jobert, Severin
TITLE OF INVENTION: FULL-LENGTH HUMAN CDNA5 ENCODING POTENTIALLY SECRETED PROTEINS
FILE REFERENCE: 78, US3, REG
CURRENT APPLICATION NUMBER: US/09/731,872
PRIOR FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/169,629
PRIOR FILING DATE: 1999-12-08
PRIOR APPLICATION NUMBER: US 60/187,470
PRIOR FILING DATE: 2000-03-06
NUMBER OF SEQ ID NOS: 482
SOFTWARE: Patent.pm
SEQ ID NO 291
LENGTH: 207
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -23...-1
US-09-731-872-291

Query Match 99.6%; Score 1120; DB 3; Length 207;
Best Local Similarity 99.5%; Pred. No. 2,9e-111;
Matches 206; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPEPLASGILLMLIAPSRACVCPHPQTAFCNSDLVIRAKFVGTPEVNOITLYOR 60
DB 1 MAPEPLASGILLMLIAPSRACVCPHPQTAFCNSDLVIRAKFVGTPEVNOITLYOR 60
QY 61 YEIMTKMYKGFQALGDAADIRFYVTPAMESVCGYFHRSHNRSEFLIAGKLODGLHIT 120
DB 61 YEIMTKMYKGFQALGDAADIRFYVTPAMESVCGYFHRSHNRSEFLIAGKLODGLHIT 120
QY 121 TCSFVAWPNWSLSLAQRGFTKTYVGCSECTVFPCLSIIPCKLOSGTHCLMTDOLLOSEK 180
DB 121 TCSFVAWPNWSLSLAQRGFTKTYVGCSECTVFPCLSIIPCKLOSGTHCLMTDOLLOSEK 180
QY 181 GFOSRHILACLPREPGLCTWOSLSRQIA 207
DB 181 GFOSRHILACLPREPGLCTWOSLSRQIA 207

RESULT 14

US-09-876-997-291
Sequence 291, Application US/09876997
Publication No. US20030152921A1
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Bougueleret, Lydie
APPLICANT: Jobert, Severin
TITLE OF INVENTION: FULL-LENGTH HUMAN CDNA5 ENCODING POTENTIALLY SECRETED PROTEINS
FILE REFERENCE: 78, US4, CIP
CURRENT APPLICATION NUMBER: US/09/876,997
PRIOR FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 09/731,872
PRIOR FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/187,470
PRIOR FILING DATE: 2000-03-06
PRIOR APPLICATION NUMBER: US 60/169,629
PRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 482
SOFTWARE: Patent.pm
SEQ ID NO 291
LENGTH: 207
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -23...-1

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: April 10, 2006, 18:09:01 ; Search time 7.51485 Seconds

(without alignments)
859.197 Million cell updates/sec

Title: US-10-734-564-100

Perfect score: 1124
Sequence: 1 MAPPEPLASGILLMLIAP.....ACLRPEGLCTWQSLRSGIA 207

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 184161 seqs, 3119182 residues

Total number of hits satisfying chosen parameters: 184161

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /SIDSS/ptodata/2/pubppaa/US08_NEW_PUB.pep.*
2: /SIDSS/ptodata/2/pubppaa/US06_NEW_PUB.pep.*
3: /SIDSS/ptodata/2/pubppaa/US07_NEW_PUB.pep.*
4: /SIDSS/ptodata/2/pubppaa/US09_NEW_PUB.pep.*
5: /SIDSS/ptodata/2/pubppaa/US10_NEW_PUB.pep.*
6: /SIDSS/ptodata/2/pubppaa/US11_NEW_PUB.pep.*
7: /SIDSS/ptodata/2/pubppaa/US12_NEW_PUB.pep.*
8: /SIDSS/ptodata/2/pubppaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1124	100.0	207	US-11-186-284-205	Sequence 205, App
2	1124	100.0	254	US-10-821-234-861	Sequence 861, App
3	1058	94.1	197	US-11-094-519A-34	Sequence 34, App1
4	1050	93.4	211	US-11-094-519A-32	Sequence 32, App1
5	837	74.5	164	US-11-094-519A-30	Sequence 30, App1
6	830.5	73.9	160	US-11-094-519A-33	Sequence 33, App1
7	782	69.6	143	US-11-094-519A-52	Sequence 52, App1
8	601	53.5	123	US-11-094-519A-31	Sequence 31, App1
9	577	51.3	108	US-11-044-640-13	Sequence 13, App1
10	551	49.0	147	US-11-094-519A-49	Sequence 49, App1
11	526	46.8	115	US-11-094-519A-51	Sequence 51, App1
12	389.5	34.7	211	US-10-821-234-1467	Sequence 1467, App
13	232	20.6	82	US-11-094-519A-50	Sequence 50, App1
14	90.5	8.1	1963	US-10-877-346-43	Sequence 43, App1
15	80.5	7.2	304	US-11-098-686-10425	Sequence 10425, App
16	75.5	6.7	283	US-11-087-039-12235	Sequence 12235, App
17	75	6.7	259	US-10-995-561-883	Sequence 883, App
18	75	6.7	764	US-11-075-047A-4	Sequence 4, App1
19	75	6.7	767	US-11-043-693-2	Sequence 2, App1
20	75	6.7	1306	US-10-995-561-905	Sequence 905, App
21	75	6.7	1356	US-10-995-561-904	Sequence 904, App
22	75	6.7	1356	US-10-995-561-906	Sequence 906, App
23	74	6.6	764	US-11-104-110-8	Sequence 8, App1
24	74	6.6	764	US-11-104-111-28	Sequence 28, App1
25	72	6.4	285	US-11-051-720-1493	Sequence 1493, App

26	72	6.4	665	7	US-11-051-720-1497	Sequence 1497, App
27	72	6.4	782	7	US-11-051-720-1496	Sequence 1496, App
28	71.5	6.4	326	7	US-11-037-243-105	Sequence 105, App
29	71.5	6.4	473	7	US-11-075-185-12	Sequence 12, App1
30	71.5	6.4	552	6	US-10-131-826A-332	Sequence 332, App
31	71.5	6.4	552	6	US-10-973-115B-332	Sequence 332, App
32	70.5	6.3	415	7	US-11-182-946-6	Sequence 6, App1
33	70.5	6.3	933	7	US-11-075-532-2928	Sequence 2928, App
34	70.5	6.3	1588	6	US-10-453-195-2	Sequence 2, App1
35	70	6.2	651	7	US-11-198-819-22	Sequence 12741, App
36	69.5	6.2	375	7	US-11-096-568A-12741	Sequence 12741, App
37	69	6.1	1198	6	US-10-877-346-35	Sequence 35, App1
38	69	6.1	1433	7	US-11-114-962-1	Sequence 1, App1
39	68.5	6.1	424	7	US-11-098-686-10348	Sequence 10348, App
40	68.5	6.1	1419	7	US-11-114-962-3	Sequence 3, App1
41	67.5	6.0	229	7	US-11-087-099-2977	Sequence 2977, App
42	67	6.0	378	7	US-11-096-568A-9995	Sequence 9995, App
43	67	6.0	407	7	US-11-096-568A-9994	Sequence 9994, App
44	67	6.0	418	7	US-11-109-156-2	Sequence 2, App1
45	67	6.0	449	7	US-11-096-568A-9993	Sequence 9993, App

ALIGNMENTS

RESULT 1
US-11-186-284-205
; Sequence 205, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MEMO1-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 205
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-11-186-284-205
Query Match 100.0%; Score 1124; DB 7; Length 207;
Best Local Similarity 100.0%; Pred. No. 2.3e-115;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPPEPLASGILLMLIAPSRACVPPHQTAFNCNSDLVIRAKFVGTPENVQTTIYOR 60
DB 1 MAPPEPLASGILLMLIAPSRACVPPHQTAFNCNSDLVIRAKFVGTPENVQTTIYOR 60
QY YEIMTMTYKGFQALGPAADIRFYITPAMSVGCFYFRSHRSEEPFLIAGLQDGLHIT 120
DB YEIMTMTYKGFQALGPAADIRFYITPAMSVGCFYFRSHRSEEPFLIAGLQDGLHIT 120
QY 121 TCSFVAVMNSLSLAQRGFTKTYTVGCEBCECTVPCLSIPCLQSGTICLMTDLOQSEK 180

```

Db      121 TCSFVAPMNSLSLAQRGFTTKTYTGCECTVFPCLSTPCKLQSGTHCLMTDQLQGSSEK 180
      |||
Qy      181 GFQSRHLACLPRPGLCTWQSLRSQIA 207
      |||
Db      181 GFQSRHLACLPRPGLCTWQSLRSQIA 207

```

RESULT 2

```

US-10-821-234-861
; Sequence 861, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Iryan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andermani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Method for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 861
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-861

```

```

Query Match      100.0%; Score 1124; DB 6; Length 254;
Best Local Similarity 100.0%; Pred. No. 3e-115;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MAPFPLASGILLMLLAPSRACCTVPPHPQTAFNSDLVIRAKFVGTPVNOGTLTYOR 60
      |||
Db      48 MAPFPLASGILLMLLAPSRACCTVPPHPQTAFNSDLVIRAKFVGTPVNOGTLTYOR 107
      |||
Qy      61 YEIKMTKWKGFQALGDADIRFVYTPAMESVCGYFHSRHSNSEEFLIAGKLQDGLIHT 120
      |||
Db      108 YEIKMTKWKGFQALGDADIRFVYTPAMESVCGYFHSRHSNSEEFLIAGKLQDGLIHT 167
      |||
Qy      121 TCSFVAPMNSLSLAQRGFTTKTYTGCECTVFPCLSTPCKLQSGTHCLMTDQLQGSSEK 180
      |||
Db      168 TCSFVAPMNSLSLAQRGFTTKTYTGCECTVFPCLSTPCKLQSGTHCLMTDQLQGSSEK 227
      |||
Qy      181 GFQSRHLACLPRPGLCTWQSLRSQIA 207
      |||
Db      228 GFQSRHLACLPRPGLCTWQSLRSQIA 254

```

RESULT 3

```

US-11-094-519A-34
; Sequence 34, Application US/11094519A
; Publication No. US20050281810A1
; GENERAL INFORMATION:
; APPLICANT: BERNSTEIN, Jeanne
; APPLICANT: LEVINE, Zurit
; TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
; FILE REFERENCE: 2786-0140P
; CURRENT APPLICATION NUMBER: US/11/094,519A
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US/09/695,293
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: IL 132558
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens

```

US-11-094-519A-34

```

Query Match      94.1%; Score 1058; DB 7; Length 197;
Best Local Similarity 95.2%; Pred. No. 3.6e-108;
Matches 197; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

```

```

Qy      1 MAPFPLASGILLMLLAPSRACCTVPPHPQTAFNSDLVIRAKFVGTPVNOGTLTYOR 60
      |||
Db      1 MAPFPLASGILLMLLAPSRACCTVPPHPQTAFNSDLVIRAKFVGTPVNOGTLTYOR 60
      |||
Qy      61 YEIKMTKWKGFQALGDADIRFVYTPAMESVCGYFHSRHSNSEEFLIAGKLQDGLIHT 120
      |||
Db      61 YEIKMTKWKGFQALGDADIRFVYTPAMESVCGYFHSRHSNSEEFLIAGKLQDGLIHT 110
      |||
Qy      121 TCSFVAPMNSLSLAQRGFTTKTYTGCECTVFPCLSTPCKLQSGTHCLMTDQLQGSSEK 180
      |||
Db      111 TCSFVAPMNSLSLAQRGFTTKTYTGCECTVFPCLSTPCKLQSGTHCLMTDQLQGSSEK 170
      |||
Qy      181 GFQSRHLACLPRPGLCTWQSLRSQIA 207
      |||
Db      171 GFQSRHLACLPRPGLCTWQSLRSQIA 197

```

RESULT 4

```

US-11-094-519A-32
; Sequence 32, Application US/11094519A
; Publication No. US20050281810A1
; GENERAL INFORMATION:
; APPLICANT: BERNSTEIN, Jeanne
; APPLICANT: LEVINE, Zurit
; TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
; FILE REFERENCE: 2786-0140P
; CURRENT APPLICATION NUMBER: US/11/094,519A
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US/09/695,293
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: IL 132558
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-094-519A-32

```

```

Query Match      93.4%; Score 1050; DB 7; Length 211;
Best Local Similarity 94.8%; Pred. No. 2.9e-107;
Matches 200; Conservative 1; Mismatches 6; Indels 4; Gaps 4;

```

```

Qy      1 MAPFPLASGILLMLLAPSRACCTVPPHPQTAFNSDLVIRAKFVGTPVNOGTLTYOR 60
      |||
Db      1 MAPFPLASGILLMLLAPSRACCTVPPHPQTAFNSDLVIRAKFVGTPVNOGTLTYOR 60
      |||
Qy      61 YEIKMTKWKGFQALGDADIRFVYTPAMESVCGYFHSRHSNSEEFLIAGKLQDGLIHT 118
      |||
Db      61 YEIKMTKWKGFQALGDADIRFVYTPAMESVCGYFHSRHSNSEEFLIAGKLQDGLIHT 120
      |||
Qy      119 ITTGSFV-APM-NSLSLAQRGFTTKTYTGCECTVFPCLSTPCKLQSGTHCLMTDQLQ 176
      |||
Db      121 SLTGSFCWPMWENSLSLAQRGFTTKTYTGCECTVFPCLSTPCKLQSGTHCLMTDQLQ 180
      |||
Qy      177 GSEKGFQSRHLACLPRPGLCTWQSLRSQIA 207
      |||
Db      181 GSEKGFQSRHLACLPRPGLCTWQSLRSQIA 211

```

RESULT 5

```

US-11-094-519A-30
; Sequence 30, Application US/11094519A
; Publication No. US20050281810A1
; GENERAL INFORMATION:
; APPLICANT: BERNSTEIN, Jeanne

```

APPLICANT: LEVINE, Zurit
; TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
; FILE REFERENCE: 2786-0140P
; CURRENT APPLICATION NUMBER: US/11/094,519A
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US/09/695,293
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: IL 132558
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-094-519A-30

Query Match 74.5%; Score 837; DB 7; Length 164;
Best Local Similarity 100.0%; Pred. No. 4,2e-84;
Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPEPLASGILLMLIAPSRACVCPHPQTAFCNSDVIYRAKFGVTPVNOQTLYOR 60
DB 1 MAPEPLASGILLMLIAPSRACVCPHPQTAFCNSDVIYRAKFGVTPVNOQTLYOR 60
QY 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSEBFLAGKLODGLLHIT 120
DB 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSEBFLAGKLODGLLHIT 120
QY 121 TCSFVAPMNSLSLAQRGFTKTYTGCECTVFPCL 155
DB 121 TCSFVAPMNSLSLAQRGFTKTYTGCECTVFPCL 155

RESULT 6
US-11-094-519A-33
; Sequence 33, Application US/11094519A
; Publication No. US20050281810A1
; GENERAL INFORMATION:
; APPLICANT: BERNSTEIN, Jeanne
; APPLICANT: LEVINE, Zurit
; TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
; FILE REFERENCE: 2786-0140P
; CURRENT APPLICATION NUMBER: US/11/094,519A
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US/09/695,293
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: IL 132558
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-094-519A-33

Query Match 73.9%; Score 830.5; DB 7; Length 160;
Best Local Similarity 77.3%; Pred. No. 2,1e-83;
Matches 160; Conservative 0; Mismatches 0; Indels 47; Gaps 1;

QY 1 MAPEPLASGILLMLIAPSRACVCPHPQTAFCNSDVIYRAKFGVTPVNOQTLYOR 60
DB 1 MAPEPLASGILLMLIAPSRACVCPHPQTAFCNSDVIYRAKFGVTPVNOQTLYOR 60
QY 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSEBFLAGKLODGLLHIT 120
DB 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSEBFLAGKLODGLLHIT 120
QY 121 TCSFVAPMNSLSLAQRGFTKTYTGCECTVFPCL 180
DB 109 -----LSIPCKLQSGTHCLMTDQLQSGSEK 133

QY 181 GFOSRHIACTPREPGICTWQSLSQIA 207
DB 134 GFOSRHIACTPREPGICTWQSLSQIA 160

RESULT 7
US-11-094-519A-52
; Sequence 52, Application US/11094519A
; Publication No. US20050281810A1
; GENERAL INFORMATION:
; APPLICANT: BERNSTEIN, Jeanne
; APPLICANT: LEVINE, Zurit
; TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
; FILE REFERENCE: 2786-0140P
; CURRENT APPLICATION NUMBER: US/11/094,519A
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US/09/695,293
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: IL 132558
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-094-519A-52

Query Match 69.6%; Score 782; DB 7; Length 143;
Best Local Similarity 100.0%; Pred. No. 3,7e-78;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 MTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSEBFLAGKLODGLLHITTCSP 124
DB 1 MTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSEBFLAGKLODGLLHITTCSP 60
QY 125 VAPMNSLSLAQRGFTKTYTGCECTVFPCLISTPCKLOSGTHCLMTDQLQSGSEK 184
DB 61 VAPMNSLSLAQRGFTKTYTGCECTVFPCLISTPCKLOSGTHCLMTDQLQSGSEK 120
QY 185 RHIACTPREPGICTWQSLSQIA 207
DB 121 RHIACTPREPGICTWQSLSQIA 143

RESULT 8
US-11-094-519A-31
; Sequence 31, Application US/11094519A
; Publication No. US20050281810A1
; GENERAL INFORMATION:
; APPLICANT: BERNSTEIN, Jeanne
; APPLICANT: LEVINE, Zurit
; TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
; FILE REFERENCE: 2786-0140P
; CURRENT APPLICATION NUMBER: US/11/094,519A
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US/09/695,293
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: IL 132558
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-094-519A-31

Query Match 53.5%; Score 601; DB 7; Length 123;
Best Local Similarity 100.0%; Pred. No. 1,9e-58;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPEPLASGILLMLIAPSRACVCPHPQTAFCNSDVIYRAKFGVTPVNOQTLYOR 60

Db 1 MAPFEPLASGILLMLLAPSRACCTVPPHPQTAFCSNDSLVIKAFVGTPEVNOQTTLXOR 60
QY 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSEEFLLI 113
Db 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSEEFLLI 113

RESULT 9

US-11-044-640-13
; Sequence 13, Application US/11044640
; Publication No. US2006002969A1
; GENERAL INFORMATION:
; APPLICANT: Kyriakides, Themis
; APPLICANT: Bornstein, Paul
; TITLE OF INVENTION: METHODS FOR REDUCING THE FOREIGN BODY REACTION
; FILE REFERENCE: UMOT1124322
; CURRENT APPLICATION NUMBER: US/11/044,640
; CURRENT FILING DATE: 2005-01-26
; PRIOR APPLICATION NUMBER: US 60/539,821
; PRIOR FILING DATE: 2004-01-27
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-044-640-13

Query Match 51.3%; Score 577; DB 7; Length 108;
Best Local Similarity 100.0%; Pred. No. 6,9e-56;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPFEPLASGILLMLLAPSRACCTVPPHPQTAFCSNDSLVIKAFVGTPEVNOQTTLXOR 60
Db 1 MAPFEPLASGILLMLLAPSRACCTVPPHPQTAFCSNDSLVIKAFVGTPEVNOQTTLXOR 60
QY 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSEEFLLI 108
Db 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSEEFLLI 108

RESULT 10

US-11-094-519A-49
; Sequence 49, Application US/11094519A
; Publication No. US20050281810A1
; GENERAL INFORMATION:
; APPLICANT: Bernstein, Jeanne
; APPLICANT: Levine, Zuriel
; TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
; FILE REFERENCE: 2786-0140P
; CURRENT APPLICATION NUMBER: US/11/094,519A
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US/09/695,293
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: IL 132558
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(147)
; OTHER INFORMATION: any Xaa is any amino acid, unknown, or other
US-11-094-519A-49

Query Match 49.0%; Score 551; DB 7; Length 147;
Best Local Similarity 68.4%; Pred. No. 7e-53;
Matches 119; Conservative 3; Mismatches 20; Indels 32; Gaps 6;

QY 1 MAPFEPLASGILLMLLAPSRACCTVPPHPQTAFCSNDSLVIKAFVGTPEVNOQTTLXOR 60
Db 1 MAPFEPLASGILLMLLAPSRACCTVPPHPQTAFCSNDSLVIKAFVGTPEVNOQTTLXOR 60
QY 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSEEFLLI 120
Db 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSEEFLLI 108

QY 121 TCSFVAPMNSLSIA---ORAGFTKTYTGCCECTVFPCLSIKCLQSGTHCLM 170
Db 109 -CWKTRGW---TLAHYILOFRGSLIO-----PELSSAPGLHQLDLC-W 146

RESULT 11

US-11-094-519A-51
; Sequence 51, Application US/11094519A
; Publication No. US20050281810A1
; GENERAL INFORMATION:
; APPLICANT: Bernstein, Jeanne
; APPLICANT: Levine, Zuriel
; TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
; FILE REFERENCE: 2786-0140P
; CURRENT APPLICATION NUMBER: US/11/094,519A
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US/09/695,293
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: IL 132558
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-094-519A-51

Query Match 46.8%; Score 526; DB 7; Length 115;
Best Local Similarity 100.0%; Pred. No. 2.8e-50;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPFEPLASGILLMLLAPSRACCTVPPHPQTAFCSNDSLVIKAFVGTPEVNOQTTLXOR 60
Db 1 MAPFEPLASGILLMLLAPSRACCTVPPHPQTAFCSNDSLVIKAFVGTPEVNOQTTLXOR 60
QY 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHR 98
Db 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHR 98

RESULT 12

US-10-821-234-1467
; Sequence 1467, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes version 1.0
; SEQ ID NO 1467
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1467

Query Match 34.7%; Score 389.5; DB 6; Length 211;

Best Local Similarity 39.6%; Pred. No. 5e-35;
Matches 78; Conservative 38; Mismatches 66; Indels 15; Gaps 7;

QY 10 GILLIL--WLIAP--SRACVPHPPOTAFPCNSDLVIYAKFVTEPVNO---TTLYORXE 62
Db 6 GLIVLGSMSLGDWGAECTSPSPHOAFPCNSDIVIRAKVKGKLVGEGPGTIV--YT 63
QY 63 IKMTMYKGFQALGDADIRFYVTPAMESVCGYFHRSHNRSEBFLIAGLQGLHITTC 122
Db 64 IKOMMYVGFYTM--PHVQIHTIASBSLGL--KLEVNKYQYLITGVVDGKMYTGLC 118
QY 123 SFVAPWNSLSLAQRGFTKYTVVGECECTVPFCLSPCKLQSGTHCLMTDQLQSGSEKGF 182
Db 119 NFEVMDQDLTSLQRKGLMYRHLGC--NCKIKSCYLLPCPVVSNKNCIMTMDLMSNGYGY 177
QY 183 QSRHLACLPREPGCLTW 199
Db 178 QSKHYACIROKGYCSW 194

RESULT 13

US-11-094-519A-50
Sequence 50, Application US/11094519A
Publication No. US20050281810A1
GENERAL INFORMATION:
APPLICANT: BERNSTEIN, Jeanne
TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
FILE REFERENCE: 2786-0140P
CURRENT APPLICATION NUMBER: US/11/094,519A
CURRENT FILING DATE: 2005-03-31
PRIOR APPLICATION NUMBER: US/09/695,293
PRIOR FILING DATE: 2000-10-25
PRIOR APPLICATION NUMBER: IL 132558
PRIOR FILING DATE: 1999-10-25
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 50
LENGTH: 82
TYPE: PRT
ORGANISM: Homo sapiens
US-11-094-519A-50

Query Match 20.6%; Score 232; DB 7; Length 82;
Best Local Similarity 95.6%; Pred. No. 2.6e-18;
Matches 43; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 67 KMYGFOALGDADIRFYVTPAMESVCGYFHRSHNRSEBFLIAGK 111
Db 13 QMYGFOALGDADIRFYVTPAMESVCGYFHRSHNRSEBFLIAGE 57

RESULT 14

US-10-877-346-43
Sequence 43, Application US/10877346
Publication No. US20060014153A1
GENERAL INFORMATION:
APPLICANT: Gerlach, Valerie L
APPLICANT: MacDougall, John R
APPLICANT: Smithson, Glenda
APPLICANT: Miller, Isabelle
APPLICANT: Stone, David
APPLICANT: Gunther, Erik
APPLICANT: Ellerman, Karen
APPLICANT: Grosse, William M
APPLICANT: Alsobrook II, John P
APPLICANT: Lepley, Denise M
APPLICANT: Burgess, Catherine E
APPLICANT: Padigaru, Muralidhara
APPLICANT: Kekuda, Ramesh
APPLICANT: Spytek, Kimberly A
APPLICANT: Leach, Martin D
APPLICANT: Shimkets, Richard A

TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same

FILE REFERENCE: 21402-124
CURRENT APPLICATION NUMBER: US/10/877,346
CURRENT FILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US/09/964,956
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/235,631
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/235,633
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/235,808
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236,064
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236,065
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236,066
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236,135
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 60/237,434
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/238,321
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 127
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 43
LENGTH: 1963
TYPE: PRT
ORGANISM: Homo sapiens
US-10-877-346-43

Query Match 8.1%; Score 90.5; DB 6; Length 1963;
Best Local Similarity 22.4%; Pred. No. 0.39;
Matches 46; Conservative 19; Mismatches 97; Indels 43; Gaps 7;

QY 10 GILLILMIAPSRACVPHPPOTAFPCNSDLVIYAKFVTEPVNOITLYORXEIMTK-- 67
Db 448 GNLEIMLMLIGDVOCTKRAVPIDNFCGLD--INOPLOGSTPVGLTLTYTSRDMTSVA 505
QY 68 --MYKGFQAL-----GDADIRFYVTPAMESVCGYFHRSHNRSEBFLIAGLQGLHI 119
Db 506 SYVNGSVVTVGKSGKLKIRADGP-----HGQYVEMSVVLKDGSPIL 552
QY 120 TTCFVAPWNSLSLAQRGFTKYTVVGECECTVP--PCLSPCKLQSGTHCLMTDQLQGS 178
Db 553 RDMAFSIDQRLVYMSHQVTRVPESEQYTTGEGCLS-----SGDPHCGMC----- 600
QY 179 EKGQSRHLACLPREPGCLTWQSLR 203
Db 601 ----ALHNMCSRDKCQAWPEPNR 620

RESULT 15

US-11-098-686-10425
Sequence 10425, Application US/11098686
Publication No. US20060024696A1
GENERAL INFORMATION:
APPLICANT: Kapur, Vivek and Gebhart, Connie J.
TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
TITLE OF INVENTION: FROM LAMSONIA INTRACELLULARIS AND METHODS OF USING
FILE REFERENCE: 09531-128001
CURRENT APPLICATION NUMBER: US/11/098,686
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US03/31318
PRIOR FILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: US 60/416,395
PRIOR FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 11433
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10425
LENGTH: 304

TYPE: PRF
ORGANISM: Lawsonia intracellularis
US-11-098-686-10425

Query Match 7.2%; Score 80.5; DB 7; Length 304;
Best Local Similarity 24.0%; Pred. No. 0.49;
Matches 49; Conservative 21; Mismatches 67; Indels 67; Gaps 11;

```
QY 2 APFEPLASGILLMLIAPSRACCTVPPHQTAFQ--NSDLVI--RAKFWGTPENVQ-TT 56
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 24 APFRVPVPAKGL-----PPVSC--PPVPGLFQCSRNQSAVAVARRRQHVSGKKQGGK 73
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 57 LYQRYEIKMTKMYKGFQALGDADIRFVY---TPMESVCGYFHRSHNRSEFLIAGKL 112
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 74 SYER-----DIKTVLPGTGEPSVRTVYGSCEKAEYGGSYPLVGRI 114
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 113 QDGLHITTCSPVAPWNSLSLAQRGFTYTYVGCCECTVPCLSI PCKLQSGTHCLWTD 172
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 115 GO-LIHAT-----GLAGRGK-----PCRQIRTLFQKGPQSAKL 147
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 173 QLLQSEKGFQSRHLACLPRPGL 196
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 148 QTLTG--RGRKLHLPCLFRRSGL 169
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

Search completed: April 10, 2006, 18:13:21
Job time : 8.51485 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: April 10, 2006, 17:55:34 ; Search time 70.1386 Seconds

(without alignments)
2082.225 Million cell updates/sec

Title: US-10-734-564-100
Perfect score: 1124
Sequence: 1 MAPFEPLASGILLMLTLPAP.....ACLPREPLGCTWQSLRSQIA 207

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1124	100.0	207	1 TIMP1_HUMAN	P01033 homo sapien
2	1124	100.0	207	2 O6RGX5_HUMAN	O6RGX5 homo sapien
3	1124	100.0	207	2 O6RC60_PONPY	O6RC60 pongo pygma
4	1117	99.4	207	1 TIMP1_PAPCY	P49061 papio cynoc
5	1104	98.2	207	1 TIMP1_MACMU	O95K19 macaca mula
6	1000.5	89.0	188	2 O5BP21_HUMAN	O5BP21 homo sapien
7	995	88.5	207	1 TIMP1_BOVIN	P20414 bos taurus
8	967	86.0	207	1 TIMP1_PIG	P35624 sus scrofa
9	961	85.5	207	1 TIMP1_SHEEP	P50122 ovis aries
10	926	82.4	207	1 TIMP1_HORSE	O05722 equus caball
11	925	82.3	207	2 O5ENG6_RABIT	O5ENG6 oryctolagus
12	915	81.4	169	2 O5GOM2_HUMAN	O5GOM2 homo sapien
13	911	81.0	203	2 O5ENG7_RABIT	O5ENG7 oryctolagus
14	903	80.3	207	1 TIMP1_CANFA	P81546 canis famli
15	902.5	80.3	206	1 TIMP1_RABIT	P20614 oryctolagus
16	837.5	74.5	205	1 TIMP1_MOUSE	P12032 mus musculu
17	818	72.8	217	1 TIMP1_RAT	P30120 rattus norv
18	818	72.8	217	2 O53YMT_RAT	O53YMT rattus norv
19	782	69.6	143	2 O5H9A7_HUMAN	O5H9A7 homo sapien
20	633	56.3	137	2 O9MZ12_SHEEP	O9MZ12 ovis aries
21	588	52.3	136	2 O5H9B5_HUMAN	O5H9B5 homo sapien
22	543	48.3	164	2 O5H9A8_HUMAN	O5H9A8 homo sapien
23	515	44.9	114	2 O6QLW9_CANFA	O6QLW9 canis famli
24	505	44.9	114	2 O6QLW9_CANFA	O6QLW9 canis famli
25	446	39.7	108	2 O6X809_FELCA	O6X809 felis silve
26	444	39.5	96	2 O5H9B4_HUMAN	O5H9B4 homo sapien
27	420.5	37.4	220	1 TIMP2_MOUSE	P25785 mus musculu
28	420.5	37.4	220	1 TIMP2_RAT	P30121 rattus norv
29	420.5	37.4	220	2 O546U4_RAT	O546U4 rattus norv
30	420.5	37.4	220	2 O6P117_MOUSE	O6P117 mus musculu
31	416.5	37.1	220	2 O6BSJ3_MOUSE	O6BSJ3 mus musculu

32	415.5	37.0	220	1 TIMP2_HUMAN	P16035 homo sapien
33	407.5	36.3	220	1 TIMP2_CANFA	O9ETV1 canis famli
34	406	36.1	222	2 O6EIV2_XENTR	O6EIV2 xenopus tro
35	406	36.1	222	2 O6EIV2_XENTR	O6EIV2 xenopus lae
36	401.5	35.7	220	1 TIMP2_CAVPO	O9WC65 cavia porce
37	401	35.7	220	1 TIMP2_CHICK	O42146 gallus gall
38	398.5	35.5	214	1 TIMP3_SCYTO	O9WE64 scylliorhinu
39	398	35.4	220	2 O64HWE_ONCMY	O64HWE oncorhynch
40	397	35.3	220	2 O4W7T6_ORYLA	O4W7T6 oryzias lac
41	397	35.3	220	2 O4JF85_FUGRU	O4JF85 fugu rubrip
42	396.5	35.3	100	2 O6GXAS_MOUSE	O6GXAS mus musculu
43	395	35.1	220	2 O60FR5_PAGMA	O60FR5 pagrus majo
44	394.5	35.1	220	1 TIMP2_BOVIN	P16368 bos taurus
45	393	35.0	220	2 O6GLMI_XENTLA	O6GLMI xenopus lae

ALIGNMENTS

RESULT 1	ID	TIMP1_HUMAN	STANDARD	PRT	207 AA.
AC	P01033	Q14252; Q9UCU1			
DT	21-JUL-1986	(Rel. 01, Created)			
DT	21-JUL-1986	(Rel. 01, Last sequence update)			
DE	10-MAY-2005	(Rel. 47, Last annotation update)			
DE		Metalloproteinase inhibitor 1 precursor (TIMP-1) (Erythroid			
DE		metalloproteinase activity) (EPA) (Tissue inhibitor of metalloproteinases)			
DE		(Fibroblast collagenase inhibitor) (collagenase inhibitor).			
GN	Name=TIMP1; Synonyms=CLG1, TIMP1;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;				
OC	Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RX	MEDLINE=86040463; PubMed=3903517;				
RA	Doeherty A.J.F., Lyons A., Smith B.J., Wright E.M., Stephens P.E.,				
RA	Harris T.J.R., Murphy G., Reynolds J.J.;				
RT	"Sequence of human tissue inhibitor of metalloproteinases and its				
RT	identity to erythroid-potentiating activity.";				
RL	Nature 318:66-69(1985).				
RN	[2]				
RP	NUCLEOTIDE SEQUENCE.				
RX	MEDLINE=85240567; PubMed=3839290;				
RA	Gaesson J.C., Golde D.W., Kaufman S.B., Westbrook C.A., Hewick R.M.,				
RA	Kaufman R.J., Wong G.G., Temple P.A., Leary A.C., Brown E.L.,				
RA	Orr E.C., Clark S.C.;				
RT	"Molecular characterization and expression of the gene encoding human				
RT	erythroid-potentiating activity.";				
RL	Nature 315:768-771(1985).				
RN	[3]				
RP	NUCLEOTIDE SEQUENCE (mRNA).				
RX	MEDLINE=86205964; PubMed=3010309;				
RA	Carmichael D.F., Sommer A., Thompson R.C., Anderson D.C., Smith C.G.,				
RA	Wegus H.G., Stricklin G.P.;				
RT	"Primary structure and cDNA cloning of human fibroblast collagenase				
RT	inhibitor.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 83:2407-2411(1986).				
RN	[4]				
RP	NUCLEOTIDE SEQUENCE.				
RA	Kazorek R.E., Honore N., Ribes V., Dehoux P., Cornet P., Cartwright T.,				
RA	Strecek R.E.;				
RT	"Molecular cloning and synthesis of biologically active human tissue				
RT	inhibitor of metalloproteinases in yeast.";				
RL	Biotechnology (N.Y.) 5:595-598(1987).				
RN	[5]				
RP	NUCLEOTIDE SEQUENCE (mRNA).				
RC	TISSUE=Ovary;				
RX	MEDLINE=91025550; PubMed=2171551;				
RA	Rapp G., Freudenstein J., Klaudiny J., Mucha J., Wempe F., Zimmer M.,				
RA	Scheit K.H.;				

RT "Characterization of three abundant mRNAs from human ovarian granulosa
 RT cells.";
 RT DNA Cell Biol. 9:479-485(1990).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=94123576; PubMed=7507419;
 RA Opbroek A., Kenney M.C., Brown D.;
 RT "Characterization of a human corneal metalloproteinase inhibitor
 RT (TIMP-1).";
 RL Curr. Res. 12:877-883(1993).
 RN [7]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 KC TISSUE=serix;
 RX MEDLINE=22188257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strunberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loggani N.A., Peters G.J., Abramson R.D., Mallory S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [8]
 RP NUCLEOTIDE SEQUENCE OF 42-207.
 RA Matsuda T., Kohno K., Kuwano M.;
 RL Submitted (JUL-1992) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP NUCLEOTIDE SEQUENCE OF 1-40.
 RA Hardcastle A.J.;
 RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
 RN [10]
 RP DISULFIDE BONDS, AND PARTIAL PROTEIN SEQUENCE.
 RX MEDLINE=90303199; PubMed=2163605;
 RA Williamson R.A., Watson P.A.O., Angal S., Koklitis P., Panico M.,
 RA Morris H.R., Carne A.F., Smith B.J., Harris T.J.R., Freedman R.B.;
 RT "Disulfide bond assignment in human tissue inhibitor of
 RT metalloproteinases (TIMP).";
 RL Biochem. J. 268:267-274(1990).
 RN [11]
 RP PROTEIN SEQUENCE OF 24-38.
 RC TISSUE=Synovial fluid;
 RX MEDLINE=92111776; PubMed=1730286; DOI=10.1016/0014-5793(92)80393-U;
 RA Ostlun A., Knauper V., Oberthof R., Reinke H., Teichgraber H.;
 RT "Isolation and characterization of tissue inhibitors of
 RT metalloproteinases (TIMP-1 and TIMP-2) from human rheumatoid synovial
 RT fluid.";
 RL FEBS Lett. 296:16-20(1992).
 RN [12]
 RP PROTEIN SEQUENCE OF 24-52.
 RX MEDLINE=91555647; PubMed=1653055; DOI=10.1016/1043-4666(91)90021-5;
 RA van Ranst M., Norga K., Masure S., Proost P., Vandekerckhove F.,
 RA Auwerx J., van Damme J., Opdenacker G.;
 RT "The cytokine-protease connection: identification of a 96-kD THP-1
 RT gelatinase and regulation by interleukin-1 and cytokine inducers.";
 RL Cytokine 3:231-239(1991).
 RN [13]
 RP PROTEIN SEQUENCE OF 24-38.
 RX PubMed=15340161; DOI=10.1110/ps.04682504;
 RA Zhang Z., Henzel W.J.;
 RT "Signal peptide prediction based on analysis of experimentally
 RT verified cleavage sites.";

RL Protein Sci. 13:2819-2824(2004).
 RN [14]
 RP MUTAGENESIS.
 RX MEDLINE=93041700; PubMed=1420137;
 RA O'Shea M., Willendroff F., Williamson R.A., Cockett M.I.,
 RA Freedman R.B., Reynolds J.J., Docherty A.J.P., Murphy G.;
 RT "Site-directed mutations that alter the inhibitory activity of the
 RT tissue inhibitor of metalloproteinases-1: importance of the N-terminal
 RT region between cysteine 3 and cysteine 13.";
 RL Biochemistry 31:10146-10152(1992).
 RN [15]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH MMP-3.
 RX MEDLINE=97433330; PubMed=9288970; DOI=10.1038/37995;
 RA Gomez-Rueth F.-X., Maslos K., Betz M., Bernger A., Huber R.,
 RA Suzuki K., Yoshida N., Nagase H., Brew K., Bourenkov G.P.,
 RA Barunk H., Bode W.;
 RT "Mechanism of inhibition of the human matrix metalloproteinase
 RT stromelysin-1 by TIMP-1.";
 RL Nature 389:77-81(1997).
 RN [16]
 RP STRUCTURE BY NMR OF 24-149.
 RX MEDLINE=20090931; PubMed=10623524; DOI=10.1006/jmbi.1999.3362;
 RA Wu B., Arunugam S., Gao G., Lee G.I., Semchenko V., Huang W.,
 RA Brew K., Van Doren S.R.;
 RT "NMR structure of tissue inhibitor of metalloproteinases-1 implicates
 RT localized induced fit in recognition of matrix metalloproteinases.";
 RL J. Mol. Biol. 295:257-268(2000).
 CC -1- FUNCTION: Complexes with metalloproteinases (such as collagenases)
 CC and irreversibly inactivates them. Also mediates erythropoiesis in
 CC vitro; but, unlike IL-3, it is species-specific, stimulating the
 CC growth and differentiation of only human and murine erythroid
 CC progenitors. Known to act on MMP-1, MMP-2, MMP-3, MMP-7, MMP-8,
 CC MMP-9, MMP-10, MMP-11, MMP-12, MMP-13 and MMP-16. Does not act on
 CC MMP-14.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: The activity of TIMP1 is dependent on the presence of
 CC disulfide bonds.
 CC -1- SIMILARITY: Belongs to the TIMP family.
 CC -1- SIMILARITY: Contains 1 NTR domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL, X03124; CAA26902.1; -; mRNA.
 DR EMBL, M12670; AAA52436.1; -; mRNA.
 DR EMBL, X02598; CAA26443.1; -; mRNA.
 DR EMBL, M59906; AAA63234.1; -; mRNA.
 DR EMBL, S68252; AAD14009.1; -; mRNA.
 DR EMBL, BC000866; AAH00866.1; -; mRNA.
 DR EMBL, D11139; BAA01913.1; -; Genomic DNA.
 DR EMBL, L47361; AAY5558.1; -; Genomic DNA.
 DR EMBL, A10416; CAA00898.1; -; Unassigned RNA.
 DR PIR, A93372; ZYHUP.
 DR PDB, 1D2B; NMR; A=24-149.
 DR PDB, 1LON; Model; A=1-207.
 DR PDB, 1O09; NMR; B=24-149.
 DR PDB, 1DEA; X-ray; B/D=24-207.
 DR GlyscoSiteDB, P01033; -;
 DR Ensemble, ENSG0000102265; Homo sapiens.
 DR HGNC, HGNC:11820; TIMP1.
 DR H-InvDB, HIX0016764; -;
 DR MIM, 305370; -;
 DR GO, GO:0005576; Extracellular region; NAS.
 DR GO, GO:0008191; Fmetalloendopeptidase inhibitor activity; IDA.
 DR GO, GO:0051045; P:negative regulation of membrane protein etc.; IDA.
 DR GO, GO:0008284; P:positive regulation of cell proliferation; TAS.
 DR InterPro, IPR001134; Netrin C
 DR InterPro, IPR001820; Prot_inh_TIMP.
 DR PANTHER, PTHR11844; Prot_inh_TIMP; 1.
 DR Pfam, PF00965; TIMP; 1.

DR PROSITE; PS50189; NTR; 1.
DR PROSITE; PS00288; TIMP; 1.

Query Match 100.0%; Score 1124; DB 1; Length 207;
Best Local Similarity 100.0%; Pred. No. 5.5e-104;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPEPLASGILLMLIAPSRACVPPHPQTAFCNSDLVIRAKFVGTPENVNQTLYOR 60
DB 1 MAPEPLASGILLMLIAPSRACVPPHPQTAFCNSDLVIRAKFVGTPENVNQTLYOR 60

QY 61 YEIKMTKMYKGFQALGDAADIRFYVTPAMESVCGYFHRSHNRSEEFLLAGKLDGLHIT 120
DB 61 YEIKMTKMYKGFQALGDAADIRFYVTPAMESVCGYFHRSHNRSEEFLLAGKLDGLHIT 120

QY 121 TCSFVAPWNSLSLAQRGFTKTYTVGCEBCTVFPCLSIIPCKLQSGTHCLMTDQLQSGSEK 180
DB 121 TCSFVAPWNSLSLAQRGFTKTYTVGCEBCTVFPCLSIIPCKLQSGTHCLMTDQLQSGSEK 180

QY 181 GFQSRHLACLPREPGLCTWOSLRQIA 207
DB 181 GFQSRHLACLPREPGLCTWOSLRQIA 207

RESULT 2
Q6FGX5 HUMAN PRELIMINARY; PRT; 207 AA.
ID Q6FGX5
AC Q6FGX5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE TIMP1 protein (Tissue inhibitor of metalloproteinase 1) (Erythroid
potentiating activity, collagenase inhibitor).
GN Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Halleck A., Ebert L., Moundinya M., Schick M., Eisenstein S.,
RA Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,
RA Korn B., Zhu D., Hu Y., Labaer J.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
RT "Cloning of human full open reading frames in Gateway(TM) system entry
RT vector (pDONR201).";
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Wray P.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR511982; CAG46779.1; -; mRNA.
DR EMBL; CR407638; CAG28566.1; -; mRNA.
DR EMBL; Z84466; CA142465.1; -; Genomic_DNA.
DR SMR; Q6FGX5; 24-204.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0008191; F:metalloendopeptidase inhibitor activity; IEA.
DR InterPro; IPR001134; Netrin_C.
DR InterPro; IPR001820; Prot_inh_TIMP.
DR Pfam; PF00965; TIMP; 1.
DR SMART; SM00206; NTR; 1.
DR PROSITE; PS50189; NTR; 1.
DR PROSITE; PS00288; TIMP; 1.
KW Collagen.
SQ SEQUENCE 207 AA; 23171 MW; 5AB4F90FFAB2ECDC CRC64;

Query Match 100.0%; Score 1124; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 5.5e-104;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPEPLASGILLMLIAPSRACVPPHPQTAFCNSDLVIRAKFVGTPENVNQTLYOR 60
DB 1 MAPEPLASGILLMLIAPSRACVPPHPQTAFCNSDLVIRAKFVGTPENVNQTLYOR 60

QY 61 YEIKMTKMYKGFQALGDAADIRFYVTPAMESVCGYFHRSHNRSEEFLLAGKLDGLHIT 120
DB 61 YEIKMTKMYKGFQALGDAADIRFYVTPAMESVCGYFHRSHNRSEEFLLAGKLDGLHIT 120

QY 121 TCSFVAPWNSLSLAQRGFTKTYTVGCEBCTVFPCLSIIPCKLQSGTHCLMTDQLQSGSEK 180
DB 121 TCSFVAPWNSLSLAQRGFTKTYTVGCEBCTVFPCLSIIPCKLQSGTHCLMTDQLQSGSEK 180

QY 181 GFQSRHLACLPREPGLCTWOSLRQIA 207
DB 181 GFQSRHLACLPREPGLCTWOSLRQIA 207

RESULT 3
Q5RC60 PONPY PRELIMINARY; PRT; 207 AA.
ID Q5RC60
AC Q5RC60;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein DKFZp468A0912;
GN Name=DKFZp468A0912;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Pongo.
NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart;
RG The German cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schnupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., And C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR858421; CAH90650.1; -; mRNA.
DR SMR; Q5RC60; 24-204.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0008191; F:metalloendopeptidase inhibitor activity; IEA.
DR InterPro; IPR001134; Netrin_C.
DR InterPro; IPR001820; Prot_inh_TIMP.
DR Pfam; PF00965; TIMP; 1.
DR SMART; SM00206; NTR; 1.
DR PROSITE; PS50189; NTR; 1.
DR PROSITE; PS00288; TIMP; 1.
KW Hypothetical protein.
SQ SEQUENCE 207 AA; 23171 MW; 5AB4F90FFAB2ECDC CRC64;

Query Match 100.0%; Score 1124; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 5.5e-104;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPEPLASGILLMLIAPSRACVPPHPQTAFCNSDLVIRAKFVGTPENVNQTLYOR 60
DB 1 MAPEPLASGILLMLIAPSRACVPPHPQTAFCNSDLVIRAKFVGTPENVNQTLYOR 60

QY 61 YEIKMTKMYKGFQALGDAADIRFYVTPAMESVCGYFHRSHNRSEEFLLAGKLDGLHIT 120
DB 61 YEIKMTKMYKGFQALGDAADIRFYVTPAMESVCGYFHRSHNRSEEFLLAGKLDGLHIT 120

QY 121 TCSFVAPWNSLSLAQRGFTKTYTVGCEBCTVFPCLSIIPCKLQSGTHCLMTDQLQSGSEK 180
DB 121 TCSFVAPWNSLSLAQRGFTKTYTVGCEBCTVFPCLSIIPCKLQSGTHCLMTDQLQSGSEK 180

QY 181 GFQSRHLACLPREPGLCTWOSLRQIA 207
DB 181 GFQSRHLACLPREPGLCTWOSLRQIA 207

RESULT 4

TIMP1_PAPCY

ID TIMP1_PAPCY STANDARD; PRT: 207 AA.

AC P49061;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Metalloproteinase inhibitor 1 precursor (TIMP-1).

GN Name=TIMP1;

OS Papio cynocephalus (yellow baboon).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

OC Cercopitheidae; Cercopithecinae; Papio.

OX NCBI_TaxId=9556;

RN [1]

RP NUCLEOTIDE SEQUENCE [MRNA].

RC TISSUE=Horta;

RA MEDLINE=96011646; PubMed=7590279; DOI=10.1016/0378-1119(95)00343-5;

RA Forough R., Nikkari S.T., Hasenstab D., Lea H., Clowes A.W.;

RT "Cloning and characterization of a cDNA encoding the baboon tissue

RT inhibitor of matrix metalloproteinase-1 (TIMP-1).";

RL Gene 163:267-271(1995).

CC -1- FUNCTION: Complexes with metalloproteinases (such as collagenases)

CC and irreversibly inactivates them.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- PTM: The activity of TIMP1 is dependent on the presence of

CC disulfide bonds.

CC -1- SIMILARITY: Belongs to the TIMP family.

CC -1- SIMILARITY: Contains 1 NTR domain.

CC -----

CC This Swiss-Prot entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use as long as its content is in no way modified and this statement is not

CC removed.

CC -----

CC EMBL; L37295; AAA99943.1; -; mRNA.

DR HSSP; P01033; 1009.

DR SMR; P49061; 24-204.

DR InterPro; IPR001134; Netrin C.

DR InterPro; IPR001820; Prot_inh_TIMP.

DR PANTHER; PTHR11844; Prot_inh_TIMP; 1.

DR Pfam; PF00965; TIMP; 1.

DR PROSITE; PSS0189; NTR; 1.

DR PROSITE; PSS0288; TIMP; 1.

KW Erythrocyte maturation; Glycoprotein; Metalloenzyme inhibitor;

KW Metalloproteinase inhibitor; Signal.

FT SIGNAL 1 23

FT CHAIN 1 23

FT DOMAIN 24 207

FT CARBOHYD 53 53

FT CARBOHYD 101 101

FT DISULFID 24 93

FT DISULFID 26 122

FT DISULFID 36 147

FT DISULFID 150 197

FT DISULFID 155 160

FT DISULFID 168 189

FT DISULFID 168 189

FT DISULFID 168 189

FT DISULFID 168 189

FT DISULFID 168 189

FT DISULFID 168 189

FT DISULFID 168 189

FT DISULFID 168 189

FT DISULFID 168 189

FT DISULFID 168 189

FT DISULFID 168 189

FT DISULFID 168 189

FT DISULFID 168 189

FT DISULFID 168 189

FT DISULFID 168 189

FT DISULFID 168 189

FT DISULFID 168 189

FT DISULFID 168 189

FT DISULFID 168 189

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

121 TCSPVAPMNSLSLAQRGFTKTYVCECTVFPCLSIPICKLQSGTHCLMTDOLLQSGSEK 180

```

Db 1 MAPEPLASGILLMLLAPSRACVLPHPQTAFCNSDLVIRAKVGFPEVNOGTLTYR 60
QY 61 YEIKRTKTKYKGFQALGDADADIRFVYTPPAMESVCGYFHRSHNRSEEFLLIAGKLODGLLHT 120
Db 61 YEIKRTKTKYKGFQALGDADADIRFVYTPPAMESVCGYFHRSHNRSEEFLLIAGKLODGLLHT 120
QY 121 TCSFVAPMNSLSLAORRGFTKTYTGCECTVFPCLSIPTCKOSGTHCLMTDQLQSGSEK 180
Db 121 TCSFVAPMNSLSLAORRGFTKTYTGCECTVFPCLSIPTCKOSGTHCLMTDQLQSGSEK 180
QY 181 GFQSRHLACTPREPGCTWQSLRSQIA 207
Db 181 GFQSRHLACTPREPGCTWQSLRTMA 207

RESULT 6
Q58P21 HUMAN
ID Q58P21 HUMAN PRELIMINARY; PRT; 188 AA.
AC Q58P21;
DT 10-MAY-2005 (TREMBLrel. 30, Created)
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
DE Tissue inhibitor of metalloproteinase 1 (Fragment).
GN Name=TIMP1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22383613; PubMed=12496489;
RA Wang M., Hu Y., Shima I., Stearns M.E.;
RT "IL-10/IL-10 receptor signaling regulates TIMP-1 expression in primary
RT human prostate tumor lines."
RL Cancer Biol. Ther. 1:556-563(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98451715; PubMed=9778693;
RA Wang M., Hu Y., Shima I., Stearns M.E.;
RT "Identification of positive and negative regulator elements for the
RT tissue inhibitor of metalloproteinase 1 gene."
RL Oncol. Res. 10:219-233(1998).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Wang M., Hu Y., Stearns M.E.;
RL Submitted (FEB-2005) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY932824; AAX47478.1; -; Genomic_DNA.
DR SMR; O58P21; 24-187.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0008191; F:metalloendopeptidase inhibitor activity; IEA.
DR InterPro; IPR001134; Netrin_C.
DR InterPro; IPR001820; Prot_inh_TIMP.
DR Pfam; PF00965; TIMP; 1.
DR SMART; SM00206; NTR; 1.
DR PROSITE; PS50189; NTR; 1.
DR PROSITE; PS00288; TIMP; 1.
FT NON_TER 188
SQ SEQUENCE 188 AA; 20917 MW; DCD275A3ADB6AC7 CRC64;

Query Match 89.0%; Score 1000.5; DB 2; Length 188;
Best Local Similarity 97.9%; Pred. No. 1.1e-91;
Matches 186; Conservative 1; Mismatches 0; Indels 3; Gaps 1;

```

```

QY 121 TCSFVAPMNSLSLAORRGFTKTYTGCECTVFPCLSIPTCKOSGTHCLMTDQLQSGSEK 180
Db 118 TCSFVAPMNSLSLAORRGFTKTYTGCECTVFPCLSIPTCKOSGTHCLMTDQLQSGSEK 177
QY 181 GFQSRHLACT 190
Db 178 GFQSRHLACT 187

RESULT 7
TIMP1 BOVIN
ID TIMP1 BOVIN STANDARD; PRT; 207 AA.
AC P20414; O53ZP2; G9TVB0;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Metalloproteinase inhibitor 1 precursor (TIMP-1) (Embryogenin-1) (EG-
DE 1).
GN Name=TIMP1;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=90365711; PubMed=2393392;
RA Freudenstein J., Wagner S., Luck R.M., Binspanier R., Scheit K.H.;
RA "RNA of bovine tissue inhibitor of metalloproteinase: sequence and
RT expression in bovine ovarian tissue."
RL Biochem. Biophys. Res. Commun. 171:250-256(1990).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=94257757; PubMed=8199264;
RA Satoh T., Kobayashi K., Yamashita S., Kikuchi M., Sendai Y., Hoshi H.;
RA "Tissue inhibitor of metalloproteinases (TIMP-1) produced by granulosa
RT and oviduct cells enhances in vitro development of bovine embryo."
RL Biol. Reprod. 50:835-844(1994).
RN [3]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC Tissue=Adrenal cortex;
RA Reichenstein M., Reich R., Lehoux J.-G., Hanukoglu I.;
RT "ACTH induces TIMP-1 expression and inhibits collagenase in adrenal
RT cortex cells."
RL Mol. Cell. Endocrinol. 215:109-114(2004).
RN [4]
RP NUCLEOTIDE SEQUENCE [MRNA] OF 25-191.
RC Tissue=Skeletal muscle;
RA Balcerzak D., Queregeesser L., Dixon W.T., Baracos V.E.;
RT "Involvement of fibroblasts and muscle cells in the expression of an
RT extracellular proteolytic cascade in bovine skeletal muscle."
RL Submitted (APR-1999) to the EMBL/Genbank/DBJ databases.
RN [5]
RP PRELIMINARY PROTEIN SEQUENCE OF 24-69.
RX MEDLINE=90008914; PubMed=2551903;
RA de Clerck Y.A., Yean T.D., Ratzkin B.J., Lu H.S., Langley K.E.;
RT "Purification and characterization of two related but distinct
RT metalloproteinase inhibitors secreted by bovine aortic endothelial
RT cells."
RL J. Biol. Chem. 264:17445-17453(1989).
RN [6]
RP FUNCTION: Complexes with metalloproteinases (such as collagenases)
RP and irreversibly inactivates them.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: The activity of TIMP1 is dependent on the presence of
CC disulfide bonds.
CC -!- SIMILARITY: Belongs to the TIMP family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

```

```

CC -----
DR EMBL; M60078.1; -; mRNA.
DR EMBL; S70841; AAB30784.1; -; mRNA.
DR EMBL; AY295346; AAP4413.1; -; mRNA.
DR EMBL; AF144763; AAD30303.1; -; mRNA.
DR FIR; A35685; A35685.
DR HSP; P01033; 1UEA.
DR SMR; P20414; 24-204.
DR InterPro; IPR001134; Netrin C.
DR InterPro; IPR001820; Prot_inh_TIMP.
DR PANTHER; PTHR11844; Prot_inh_TIMP; 1.
DR Pfam; PF00965; TIMP; 1.
DR PROSITE; PS00189; NTR; 1.
DR PROSITE; PS00288; TIMP; 1.
DR Direct protein sequencing; Erythrocyte maturation; Glycoprotein;
KW Metalloenzyme inhibitor; Metalloprotease inhibitor; Signal.
FT SIGNAL 1 23
FT CHAIN 1 23
FT DOMAIN 24 207
FT CARBOHYD 53 53
FT CARBOHYD 101 101
FT DISULFID 24 93
FT DISULFID 26 122
FT DISULFID 36 147
FT DISULFID 150 197
FT DISULFID 155 160
FT DISULFID 168 189
SQ SEQUENCE 207 AA; 23032 MW; E672BEE2865F7 CRC64;

Query Match 88.5%; Score 995; DB 1; Length 207;
Best Local Similarity 87.0%; Pred. No. 4.4e-91;
Matches 180; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

QY 1 MAPFEPLASGIIILLMLIPSRACCTVPPHPOTAFPCNSDLVIRAKVGPEVNOTTLVYR 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 MAFPAWASGIIILLMLIPSRACCTVPPHPOTAFPCNSDLVIRAKVGPEVNOTTLVYR 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 YEIKMTKMYKGFQALGDADDIRFVYTPAMESVCGYFHRSHNSEFLIAGKIQDGLLHT 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61 YEIKMTKMYKGFQALGDADDIRFVYTPAMESVCGYFHRSHNSEFLIAGKIQDGLLHT 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 121 TCSFVAPMNSLSIAQRGFTKTYTVCCECTVPPCLSIPECKIQTGHCIMTDLGSGSR 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 121 TCSFVAPMNSLSIAQRGFTKTYTVCCECTVPPCLSIPECKIQTGHCIMTDLGSGSR 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 121 TCSFVAPMNSLSIAQRGFTKTYTVCCECTVPPCLSIPECKIQTGHCIMTDLGSGSR 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 121 TCSFVAPMNSLSIAQRGFTKTYTVCCECTVPPCLSIPECKIQTGHCIMTDLGSGSR 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 181 GFOSRHLACLPRPGICTWOSLRQA 207
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 181 GFOSRHLACLPRPGICTWOSLRQA 207
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 8
TIMP1_PIG STANDARD; PRT; 207 AA.
ID TIMP1_PIG
AC P35624; Q9TT83; Q9TT89;
DT 01-JUN-1994 (Rel. 29, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Metalloprotease inhibitor 1 precursor (TIMP-1).
GN Name=TIMP1;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae;
OC Sus.
OC NCBI_TaxID=9823;
OX NCBI_TaxID=9823;
RN (1)
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Ovary;
RX MEDLINE=92201478; PubMed=1312961; DOI=10.1016/0303-7207(92)90196-D;
RA Tanaka T., Andoh N., Takeya T., Sato E.;
RT "Differential screening of ovarian cDNA libraries detected the
RT expression of the porcine collagenase inhibitor gene in functional
RT corpora lutea.";
RL Mol. Cell. Endocrinol. 83:65-71(1992).

```

```

RN [2]
RP NUCLEOTIDE SEQUENCE OF 34-195.
RA Wang J.Y., Baer A.E., Kraus V.B., Setton L.A.;
RT "Gene expression level of mmp3 and Timpl in intervertebral disc.";
RL Submitted (NOV-1999) to the EMBL/Genbank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE OF 37-144.
RC TISSUE=Skin;
RA Wang J.F., Boykiw R.H., Reno C.R., Hart D.A., Olson M.E.;
RT "Cloning and sequencing of porcine TIMPs.";
RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: Complexes with metalloproteinases (such as collagenases)
CC and irreversibly inactivates them.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: The activity of TIMP1 is dependent on the presence of
CC disulfide bonds.
CC -1- SIMILARITY: Belongs to the TIMP family.
CC -1- SIMILARITY: Contains 1 NTR domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; S96211; AAB21865.1; -; mRNA.
DR EMBL; AF201726; AAF24348.1; -; mRNA.
DR EMBL; AF156029; AAF17354.1; -; mRNA.
DR FIR; I47061; I47061.
DR HSP; P01033; 1UEA.
DR SMR; P35624; 24-203.
DR InterPro; IPR001134; Netrin C.
DR InterPro; IPR001820; Prot_inh_TIMP.
DR PANTHER; PTHR11844; Prot_inh_TIMP; 1.
DR Pfam; PF00965; TIMP; 1.
DR PROSITE; PS00189; NTR; 1.
DR PROSITE; PS00288; TIMP; 1.
DR Erythrocyte maturation; Glycoprotein; Metalloenzyme inhibitor;
KW Metalloprotease inhibitor; Signal.
FT SIGNAL 1 23
FT CHAIN 24 207
FT DOMAIN 24 147
FT CARBOHYD 53 53
FT CARBOHYD 101 101
FT DISULFID 24 93
FT DISULFID 26 122
FT DISULFID 36 147
FT DISULFID 150 197
FT DISULFID 155 160
FT DISULFID 168 189
FT DISULFID 34 34
FT DISULFID 37 37
FT DISULFID 41 41
FT DISULFID 59 59
FT DISULFID 86 86
FT DISULFID 141 142
SQ SEQUENCE 207 AA; 23099 MW; B04895846EB565D0 CRC64;

Query Match 86.0%; Score 967; DB 1; Length 207;
Best Local Similarity 83.6%; Pred. No. 2.8e-88;
Matches 173; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

QY 1 MAPFEPLASGIIILLMLIPSRACCTVPPHPOTAFPCNSDLVIRAKVGPEVNOTTLVYR 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 MAFPAWASGIIILLMLIPSRACCTVPPHPOTAFPCNSDLVIRAKVGPEVNOTTLVYR 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 YEIKMTKMYKGFQALGDADDIRFVYTPAMESVCGYFHRSHNSEFLIAGKIQDGLLHT 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61 YEIKMTKMYKGFQALGDADDIRFVYTPAMESVCGYFHRSHNSEFLIAGKIQDGLLHT 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 121 TCSFVAPMNSLSIAQRGFTKTYTVCCECTVPPCLSIPECKIQTGHCIMTDLGSGSR 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 121 TCSFVAPMNSLSIAQRGFTKTYTVCCECTVPPCLSIPECKIQTGHCIMTDLGSGSR 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

OY 181 GFOSRHLACLPREPGLCTWOSLR 207
 DB 181 GFOSRHLACMPREPGLCTWOSLR 207

RESULT 9

TIMEP1 SHEEP STANDARD; PRT; 207 AA.

AC P50122; 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Metalloproteinase inhibitor 1 precursor (TIMP-1).
 GN Name=TIMP1;
 OS Ovis aries (sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Caprinae; Ovis.
 OC NCBI_TaxID=9940;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Cornus luteum;
 RX MEDLINE=94102210; PubMed=8275949; DOI=10.1210/en.134.1.344;
 RA Smith G.W., Goetz T.L., Anthony R.V., Smith M.F.;
 RT "Molecular cloning of an ovine ovarian tissue inhibitor of
 metalloproteinases: oncogeny of messenger ribonucleic acid expression
 and in situ localization within preovulatory follicles and luteal
 tissue.";
 RL Endocrinology 134:344-352(1994).

CC -1- FUNCTION: Complexes with metalloproteinases (such as collagenases)
 and irreversibly inactivates them.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: The activity of TIMP1 is dependent on the presence of
 disulfide bonds.
 CC -1- SIMILARITY: Belongs to the TIMP family.
 CC -1- SIMILARITY: Contains 1 NTR domain.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.

CC EMBL, S67450; AAB29472.1; -, mRNA.
 DR PIR; I46964; I46964.
 DR HSP; P01033; IUEA.
 DR SMR; P50122; 24-203.
 DR InterPro: IPR001134; Netrin C.
 DR InterPro: IPR001820; Prot_inh_TIMP.
 DR PANTHER; PTHR11844; Prot_inh_TIMP; 1.
 DR Pfam; PF00965; TIMP; 1.
 DR PROSITE; PS00189; NTR; 1.
 DR PROSITE; PS00288; TIMP; 1.
 KM Erythrocyte maturation; Glycoprotein; Metalloenzyme inhibitor;
 KW Metalloproteinase inhibitor; Signal.
 FT SIGNAL 1 23 By similarity.
 FT CHAIN 24 207 Metalloproteinase inhibitor 1.
 FT DOMAIN 24 147 NTR.
 FT CARBOHYD 53 53 N-linked (GlcNAc . . .) (Potential).
 FT DISULFID 101 101 N-linked (GlcNAc . . .) (Potential).
 FT DISULFID 24 93 By similarity.
 FT DISULFID 26 122 By similarity.
 FT DISULFID 36 147 By similarity.
 FT DISULFID 150 197 By similarity.
 FT DISULFID 155 160 By similarity.
 FT DISULFID 168 189 By similarity.
 SQ SEQUENCE 207 AA; 23058 MW; 1D3BCA201F80B46 CRC64;

Query Match 85.5%; Score 961; DB 1; Length 207;
 Best Local Similarity 85.7%; Pred. NO. 1,le-87;
 Matches 174; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

OY 1 MAPFPLASGILLMLTAPSRACVPPHPQTAFCNSDLVIKAFVGNTPVNOTLYOR 60
 DB 1 MALPAPYSGILLMLTAPSRACVPPHPQTAFCNSDLVIKAFVGNTPVNOTLYOR 60
 OY 61 YEIKNTKMYKGFALGDAADIRFYTPPAMESVCGYFHRSHNRSEFFLAGKLDGLIHT 120
 DB 61 YEIKNTKMYKGFALGDAADIRFYTPPAMESVCGYFHRSHNRSEFFLAGKLDGLIHT 120
 OY 121 TCSFVAPWNSISLQRRGFTTYVVGCECTVPFGLSIPCKLQSGHCLMTDQLQSEBK 180
 DB 121 TCSFVAPWNSISLQRRGFTTYVVGCECTVPFGLSIPCKLQSGHCLMTDQLQSEBK 180
 OY 181 GFOSRHLACLPREPGLCTWOSLR 203
 DB 181 GFOSRHLACLPREPGLCTWOSLR 203

RESULT 10

TIMEP1 HORSE STANDARD; PRT; 207 AA.

AC O02722; 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Metalloproteinase inhibitor 1 precursor (TIMP-1).
 GN Name=TIMP1;
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
 OC NCBI_TaxID=9796;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Cartilage;
 RX MEDLINE=99074117; PubMed=9858406;
 RA Richardson D.W., Dodge G.R.;
 RT "Molecular characteristics of equine stromelysin and the tissue
 inhibitor of metalloproteinase 1.";
 RL Am. J. Vet. Res. 59:1557-1562(1998).

CC -1- FUNCTION: Complexes with metalloproteinases (such as collagenases)
 and irreversibly inactivates them (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: The activity of TIMP1 is dependent on the presence of
 disulfide bonds (By similarity).
 CC -1- SIMILARITY: Belongs to the TIMP family.
 CC -1- SIMILARITY: Contains 1 NTR domain.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.

CC EMBL; U95039; AAB53735.1; -, mRNA.
 DR HSP; P01033; IUEA.
 DR SMR; O02722; 24-203.
 DR InterPro: IPR001134; Netrin C.
 DR InterPro: IPR001820; Prot_inh_TIMP.
 DR PANTHER; PTHR11844; Prot_inh_TIMP; 1.
 DR Pfam; PF00965; TIMP; 1.
 DR PROSITE; PS00189; NTR; 1.
 DR PROSITE; PS00288; TIMP; 1.
 KM Erythrocyte maturation; Glycoprotein; Metalloenzyme inhibitor;
 KW Metalloproteinase inhibitor; Signal.
 FT SIGNAL 1 23 By similarity.
 FT CHAIN 24 207 Metalloproteinase inhibitor 1.
 FT DOMAIN 24 147 NTR.
 FT CARBOHYD 53 53 N-linked (GlcNAc . . .) (Potential).
 FT DISULFID 101 101 N-linked (GlcNAc . . .) (Potential).
 FT DISULFID 24 93 By similarity.
 FT DISULFID 26 122 By similarity.
 FT DISULFID 36 147 By similarity.
 FT DISULFID 150 197 By similarity.
 FT DISULFID 155 160 By similarity.

FT DISULFID 168 189 By similarity.
SQ SEQUENCE 207 AA; 23046 MW; FD710DA98D168070 CRC64;

Query Match 82.4%; Score 926; DB 1; Length 207;

Best Local Similarity 82.6%; Pred. No. 3,5e-84;
Matches 171; Conservative 12; Mismatches 24; Indels 0; Gaps 0;

```

QY 1 MAPPEPLASGILLMLLIPASRACVCPHPOTAFPCNSDLVIRAKVGTPEVNOGTLTYOR 60
DB 1 MAPPEPLASGILLMLLIPASRACVCPHPOTAFPCNSDLVIRAKVGTPEVNOGTLTYOR 60
QY 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSSEFLIAGKLQDGLLHIT 120
DB 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSSEFLIAGKLQDGLLHIT 120
QY 121 TCSFVAPMNSLSLAQRGFTKTYTVCCECTVFPCLSIPOKLSQSTHCLMTDQLLGSEK 180
DB 121 TCSFVAPMNSLSLAQRGFTKTYTVCCECTVFPCLSIPOKLSQSTHCLMTDQLLGSEK 180
QY 181 GFQSRHLACLPRERPGCTWQSLRPRTA 207
DB 181 GFQSRHLACLPRERPGCTWQSLRPRTA 207

```

RESULT 11

OSENG6_RABIT PRELIMINARY; PRT; 207 AA.

```

AC OSENG6;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Tissue inhibitor of metalloproteinase 1.
GN Name-TIMP-1;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Estelle J., Saetre Y., Merchán M., Folch J.M.;
RT "Characterization and sequencing of the rabbit TIMP-1 gene.";
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY829731; AAW79054.1; -; Genomic_DNA.
DR InterPro; IPR001134; Netrin_C.
DR InterPro; IPR001820; Prot_inh_TIMP.
DR Pfam; PF00965; TIMP; 1.
DR SMART; SM00206; NTR; 1.
DR PROSITE; PS50189; NTR; 1.
DR PROSITE; PS00288; TIMP; 1.
SQ SEQUENCE 207 AA; 22937 MW; FA39B19352370B5B CRC64;

```

Query Match 82.3%; Score 925; DB 2; Length 207;

Best Local Similarity 82.3%; Pred. No. 4.4e-84;
Matches 167; Conservative 12; Mismatches 24; Indels 0; Gaps 0;

```

QY 1 MAPPEPLASGILLMLLIPASRACVCPHPOTAFPCNSDLVIRAKVGTPEVNOGTLTYOR 60
DB 1 MAPPEPLASGILLMLLIPASRACVCPHPOTAFPCNSDLVIRAKVGTPEVNOGTLTYOR 60
QY 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSSEFLIAGKLQDGLLHIT 120
DB 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSSEFLIAGKLQDGLLHIT 120
QY 121 TCSFVAPMNSLSLAQRGFTKTYTVCCECTVFPCLSIPOKLSQSTHCLMTDQLLGSEK 180
DB 121 TCSFVAPMNSLSLAQRGFTKTYTVCCECTVFPCLSIPOKLSQSTHCLMTDQLLGSEK 180
QY 181 GFQSRHLACLPRERPGCTWQSLRPRTA 203
DB 181 GFQSRHLACLPRERPGCTWQSLRPRTA 203

```

RESULT 12

O96QM2_HUMAN PRELIMINARY; PRT; 169 AA.

AC O96QM2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE TIMP1 protein.

```

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Prostate;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleorn M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney U., Helton B., Kettelman M., Madan A., Rodríguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield V.S.N., Krzywinski M.I., Skalske U., Smalls D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC007097; AAH07097.1; -; mRNA.
DR HSSP; P01033; 1009.
DR SMR; O96QM2; 24-169.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0008191; F:metalloendopeptidase inhibitor activity; IEA.
DR InterPro; IPR001134; Netrin_C.
DR InterPro; IPR001820; Prot_inh_TIMP.
DR PANTHER; PTHR11844; Prot_inh_TIMP.
DR Pfam; PF00965; TIMP; 1.
DR SMART; SM00206; NTR; 1.
DR PROSITE; PS50189; NTR; 1.
DR PROSITE; PS00288; TIMP; 1.
SQ SEQUENCE 169 AA; 18847 MW; 6C164206C87D815C CRC64;

```

Query Match 81.4%; Score 915; DB 2; Length 169;

Best Local Similarity 100.0%; Pred. No. 3.4e-83;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MAPPEPLASGILLMLLIPASRACVCPHPOTAFPCNSDLVIRAKVGTPEVNOGTLTYOR 60
DB 1 MAPPEPLASGILLMLLIPASRACVCPHPOTAFPCNSDLVIRAKVGTPEVNOGTLTYOR 60
QY 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSSEFLIAGKLQDGLLHIT 120
DB 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSSEFLIAGKLQDGLLHIT 120
QY 121 TCSFVAPMNSLSLAQRGFTKTYTVCCECTVFPCLSIPOKLSQSTHCL 169
DB 121 TCSFVAPMNSLSLAQRGFTKTYTVCCECTVFPCLSIPOKLSQSTHCL 169

```



```
RESULT 13
O5ENG7 RABIT
ID O5ENG7 RABIT PRELIMINARY; PRT; 203 AA.
AC O5ENG7;
DT 10-MAY-2005 (TREMBLrel. 30, Created)
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
DE Tissue inhibitor of metalloproteinase 1 (Fragment).
GN Name=TIMP-1;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Estelle J., Sastre Y., Merchan M., Polch J.M.;
RT "Characterization and sequencing of the rabbit TIMP-1 gene.";
RL Submitted (NOV-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY829730; AAW79053.1; -; mRNA.
DR InterPro; IPR001134; Netrin C.
DR InterPro; IPR001820; Prot_inh_TIMP.
DR Pfam; PF00965; TIMP; 1.
DR SMART; SM00206; NTR; 1.
DR PROSITE; PS0189; NTR; 1.
DR PROSITE; PS00288; TIMP; 1.
FT NON TER 1
SQ SEQUENCE 203 AA; 22525 MW; ELDICEL3047AEFS CRC64;

Query Match 81.0%; Score 911; DB 2; Length 203;
Best Local Similarity 83.2%; Pred. No. 1,le-82;
Matches 164; Conservative 12; Mismatches 21; Indels 0; Gaps 0;

OY 7 LASGLLLMLIAPSRACVCPHPQTAFCNSDVIYRAKFTGTPVNTTYLQREIKMT 66
DB 3 LASSWLLMLIAPSRACVCPHPQTAFCNSDVIYRAKFTGTPVNTTYLQREIKMT 62
OY 67 KMVKGFOALGDAADIRFYTPAMESVCGYFHRSHNRSEFFLAGLQGLHITTCSPVA 126
DB 63 KMFGFDFLGHATDIRFYTPAMESVCGYSHKQNRSEFFLAGLQGLHITTCSPV 122
OY 127 PMSISLQARGFTTYTNGCECTVPCLSIPCKLQSGTHCLMTDQLQSEKGFQSRH 186
DB 123 PMSISLQARGFTTYTNGCECTVPCLSIPCKLQSGTHCLMTDQLQSEKGFQSRH 182
OY 187 LACLPREPGLCTWOSLR 203
DB 183 LACLPREPGLCTWOSLR 199

RESULT 14
TIMP1 CANFA
ID TIMP1 CANFA STANDARD; PRT; 207 AA.
AC P81546; O8TOS;
DT 15-JUL-1999 (Rel. 38, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Metalloproteinase inhibitor 1 precursor (TIMP-1).
GN Name=TIMP1;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE [mRNA].
RA STRAIN-Cocker spaniel; TISSUE=Kidney;
RA Notitake H., Miyamori H., Goto C., Seiki M., Sato H.;
RT "Overexpression of tissue inhibitor of matrix metalloproteinases-1
(TIMP-1) in metastatic MDCK cells transformed by v-src.";
RL Submitted (AUG-1998) to the EMBL/Genbank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
```

```
RX MEDLINE=99132652; PubMed=9931441; DOI=10.1016/S0378-1119(98)00521-6;
RA Zeiss C.J., Acland G.M., Aguirre G.D., Ray K.;
RT "TIMP-1 expression is increased in x-linked progressive retinal
atrophy despite its exclusion as a candidate gene.";
RL Gene 225:67-75 (1998).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=92175241; PubMed=1794505;
RA Chopra R., Koklitis P.A., Bergin S., Rowe J., Angal S.;
RT "Purification of recombinant dog tissue inhibitor of
metalloproteinases.";
RL Biochem. Soc. Trans. 19:372S-372S (1991).
CC -1- FUNCTION: Complexes with metalloproteinases (such as collagenases)
and irreversibly inactivates them.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Ubiquitously expressed. Highest expression in
kidney and ovary.
CC -1- PTM: The activity of TIMP1 is dependent on the presence of
disulfide bonds.
CC -1- SIMILARITY: Belongs to the TIMP family.
CC -1- SIMILARITY: Contains 1 NTR domain.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
-----
DR EMBL; AB016817; BAA32393.1; -; mRNA.
DR EMBL; AF077817; AAD10632.1; -; mRNA.
DR EMBL; AF079767; AAD10633.1; -; Genomic DNA.
DR HSSP; P01033; IUEA.
DR SMR; P81546; 24-203.
DR Bnemb1; ENSGAFG00000015155; Canis familiaris.
DR InterPro; IPR001134; Netrin C.
DR InterPro; IPR001820; Prot_inh_TIMP.
DR PANTHER; PTHR11844; Prot_inh_TIMP; 1.
DR Pfam; PF00965; TIMP; 1.
DR PROSITE; PS0189; NTR; 1.
DR PROSITE; PS00288; TIMP; FALSE_NEG.
KW Erythrocyte maturation; Glycoprotein; Metalloenzyme inhibitor;
KW Metalloproteinase inhibitor; Signal.
FT SIGNAL 1 23
FT CHAIN 24 207
FT DOMAIN 24 147
FT CARBOHYD 53 53
FT CARBOHYD 77 77
FT CARBOHYD 101 101
FT DISULFID 24 93
FT DISULFID 26 122
FT DISULFID 36 147
FT DISULFID 150 197
FT DISULFID 155 160
FT DISULFID 168 189
FT CONFLICT 17 17
FT CONFLICT 35 35
FT CONFLICT 173 173
FT CONFLICT 203 203
SQ SEQUENCE 207 AA; 22852 MW; D36C8A67B3B784D CRC64;

Query Match 80.3%; Score 903; DB 1; Length 207;
Best Local Similarity 79.7%; Pred. No. 6,9e-82;
Matches 165; Conservative 14; Mismatches 28; Indels 0; Gaps 0;

OY 1 MAPPEPLASGLILLMLIAPSRACVCPHPQTAFCNSDVIYRAKFTGTPVNTTYLQREIKMT 60
DB 1 MAPPEPLASGLILLMLIAPSRACVCPHPQTAFCNSDVIYRAKFTGTPVNTTYLQREIKMT 60
OY 61 YEIKMTKMYKFOALGDAADIRFYTPAMESVCGYFHRSHNRSEFFLAGLQGLHITTCSPVA 120
DB 61 YEIKMTKMYKFOALGDAADIRFYTPAMESVCGYFHRSHNRSEFFLAGLQGLHITTCSPVA 120
OY 121 TCSFVAPWNSLSLAQRGFTTYTNGCECTVPCLSIPCKLQSGTHCLMTDQLQSEK 180
```

```

Db      121 TCSFVAPNNSLSLTAQRGFTKTYTGAECCECTVFTCSIRPKQSGDTHCLMTDHLGSDK 180
QY      181 GFQSRHLACLPREPGICTWQSIRSQTA 207
Db      181 GFQSRHLACLPREPGICTWQSIRPMA 207

RESULT 15
TIMP1_RABIT STANDARD; PRT; 206 AA.
ID      TIMP1_RABIT
AC      P20614;
DT      01-FEB-1991 (Rel. 17, Created)
DT      01-FEB-1991 (Rel. 17, Last sequence update)
DT      10-MAY-2005 (Rel. 47, Last annotation update)
DE      Metalloproteinase inhibitor 1 precursor (TIMP-1).
GN      Name=TIMP1;
OS      Oryctolagus cuniculus (Rabbit).
OC      Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC      Oryctolagus.
OK      NCBI_TaxId=9986;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RX      MEDLINE=89214135; PubMed=2708356;
RA      Horowitz S., Dafni N., Shapiro D.L., Holm B.A., Nottter R.H.,
RA      Quible D.J.;
RT      "Hyperoxic exposure alters gene expression in the lung. Induction of
RT      the tissue inhibitor of metalloproteinases mRNA and other mRNAs.";
RL      J. Biol. Chem. 264:7092-7095(1989).
CC      -1- FUNCTION: Complexes with metalloproteinases (such as collagenases)
CC      and irreversibly inactivates them.
CC      -1- SUBCELLULAR LOCATION: Secreted.
CC      -1- PTM: The activity of TIMP1 is dependent on the presence of
CC      disulfide bonds.
CC      -1- SIMILARITY: Belongs to the TIMP family.
CC      -1- SIMILARITY: Contains 1 NTR domain.
CC      -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
DR      EMBL, J04712; AAA1478.1; -; mRNA.
DR      PIR, A33350; A33350.
DR      HSSP, P01033; 1009.
DR      SMR, P20614; 24-202.
DR      InterPro, IPR001134; Netrin C.
DR      InterPro, IPR001820; Prot_inh_TIMP.
DR      PANTHER, PTHR11844; Prot_inh_TIMP; 1.
DR      Pfam, PF00965; TIMP; 1.
DR      PROSITE, PS50189; NTR; 1.
DR      PROSITE, PS00288; TIMP; 1.
KW      Erythrocyte maturation; Glycoprotein; Metalloenzyme inhibitor;
KW      Metalloproteinase inhibitor; Signal.
FT      SIGNAL 1 23
FT      CHAIN 1 206
FT      DOMAIN 24 147 NTR.
FT      CARBOHYD 53 53 N-linked (GlcNAc..)(Potential).
FT      CARBOHYD 101 101 N-linked (GlcNAc..)(Potential).
FT      DISULFID 24 93 By similarity.
FT      DISULFID 26 122 By similarity.
FT      DISULFID 36 147 By similarity.
FT      DISULFID 147 196 By similarity.
FT      DISULFID 150 196 By similarity.
FT      DISULFID 155 160 By similarity.
FT      DISULFID 168 188 By similarity.
SQ      SEQUENCE 206 AA; 22758 MW; 1839A8DE7174EE9E CRC64;

Query Match 80.3%; Score 902.5; DB 1; Length 206;
Best Local Similarity 80.8%; Pred. No. 7.7e-82;
Matches 164; Conservative 13; Mismatches 25; Indels 1; Gaps 1;

```

```

QY      1 MAPFEIASGILLLLMLAPSRACCTVPPHPOTAFCSNDLVIRAKFVGTPVNNQTLTYOR 60
Db      1 MAPPLAALASSMLLLMLVAPSRACCTVPPHPOTAFCSNDLVIRAKFVGAPENVNHTLTYOR 60
QY      61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSSEFLIAGKLQDGLLHIT 120
Db      61 YEIKTTKMGKFDALGHATDIRFVYTPAMESVCGYSHKSQNSSEFLIAGQLRNGLLHIT 120
QY      121 TCSFVAPNNSLSLAQRGFTKTYTGAECCECTVFPCLSTFCKLQSGTHCLMTDQLQSGEK 180
Db      121 TCSFVAPNNSLSFSQSGFTKTYAGCDMCTVFACASIPCHLESDTHCLMTDSSL-GSDK 179
QY      181 GFQSRHLACLPREPGICTWQSIR 203
Db      180 GFQSRHLACLPREPGICAMESIR 202

```

Search completed: April 10, 2006, 18:06:34
Job time : 73.1386 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 10, 2006, 18:01:46 ; Search time 11.8416 Seconds
(without alignments)
1681.943 Million cell updates/sec

Title: US-10-734-564-100

Perfect score: 1124

Sequence: 1 MAPFPLASGILLMLLMLAP.....ACLPREPGLCTWQSLRSQIA 207

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1124	100.0	207	1 ZYHUP	metalloproteinase
2	1117	99.4	207	2 A34303	matrix metalloprot
3	995	88.5	207	1 A35685	metalloproteinase
4	971	86.4	207	2 I47061	collagenase inhibi
5	961	85.5	207	2 I46964	metalloproteinase
6	902.5	80.3	206	1 A33350	metalloproteinase
7	837.5	74.5	205	1 A26106	metalloproteinase
8	818	72.8	217	1 UC2557	metalloproteinase
9	420.5	37.4	220	1 JH0683	metalloproteinase
10	420.5	37.4	220	2 I53415	metalloproteinase
11	417.5	37.1	220	1 S45683	tissue inhibitor o
12	415.5	37.0	220	1 A37128	metalloproteinase
13	394.5	35.1	220	1 A35996	metalloproteinase
14	389.5	34.7	211	1 S45317	metalloproteinase
15	388.5	34.6	196	1 S38624	metalloproteinase
16	388.5	34.6	212	1 A43429	metalloproteinase
17	385.5	34.3	211	1 A53532	metalloproteinase
18	384.5	34.2	211	2 JC34630	metalloproteinase
19	112.5	10.0	2	1 F53728	metalloproteinase
20	94	8.4	2	2 F9123	metalloproteinase
21	86.5	7.7	7	7 B65058	protein KOTC11.5
22	86	7.7	433	1 B65058	fixC protein homol
23	83	7.4	4307	2 GQRTT1	tumor necrosis fac
24	82	7.3	454	1 GQMT1	hypothetical prote
25	81.5	7.3	1884	2 JC4975	tumor necrosis fac
26	78.5	7.0	433	2 B51081	plexin 2 precursor
27	78.5	7.0	433	2 B51081	hypothetical prote
28	78.5	7.0	724	2 G66271	hypothetical prote
29	77.5	6.9	359	1 K1BERT	protein F16A14.7

30	77.5	6.9	944	2 S66870	DNL4 protein - yea
31	76.5	6.8	183	2 A32851	22K extracellular
32	76.5	6.8	709	2 G36610	probable disease r
33	76	6.8	266	2 S02510	nifH protein - Kle
34	75.5	6.7	530	2 F84488	probable Tail-like
35	75.5	6.7	1513	2 A54895	mucin 2, intestinal
36	75	6.7	1356	2 JC1402	protein-tyrosine k
37	74.5	6.6	430	2 S73268	histidine-tyrosine
38	74.5	6.6	444	2 S48696	suppressor protein
39	73.5	6.5	259	1 P1VXTA	RNA 1 protein - hu
40	73	6.5	259	1 JC7109	STIV protein - hu
41	73	6.5	480	2 F82796	hypothetical prote
42	73	6.5	537	2 I49135	prolyl 4-hydroxyla
43	73	6.5	555	2 D71444	probable thioester
44	72.5	6.5	611	2 A83926	hypothetical prote
45	72	6.4	589	2 G71462	probable ABC trans

ALIGNMENTS

RESULT 1
ZYHUP
metalloproteinase tissue inhibitor 1 precursor [validated] - human
N:Alternate names: erythroid potentiating activity (EPA); fibroblast collagenase inhib;
C:Species: Homo sapiens (man)
C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C:Accession: A93372; A93363; A23534; A20595; A35826; A48417; S20318; S15872; I52912; S
R:DoCherty, A.J.P.; Lyons, A.; Smith, B.D.; Wright, E.M.; Stephens, P.E.; Harris, T.D.,
Nature 318, 66-69, 1985
A:Title: Sequence of human tissue inhibitor of metalloproteinases and its identity to
A:Reference number: A93372; MUID:86040463; PMID:3903517
A:Accession: A93372
A:Molecule type: mRNA
A:Residues: 1-207 <DOC>
A:Cross-references: UNIPROT:P01033; UNIPARC:UPI00001135B1; GB:X03124; NID:937182; PIDN
R:Gasson, J.C.; Golde, D.W.; Kaufman, S.E.; Westbrook, C.A.; Hewick, R.M.; Kaufman, R.,
Nature 315, 768-771, 1985
A:Title: Molecular characterization and expression of the gene encoding human erythroi
A:Reference number: A93363; MUID:85240567; PMID:3839290
A:Accession: A93363
A:Molecule type: mRNA
A:Residues: 1-207 <GAS>
A:Cross-references: UNIPARC:UPI00001135B1
R:Carimichael, D.F.; Sommer, A.; Thompson, R.C.; Anderson, D.C.; Smith, C.G.; Welgus, H
Proc. Natl. Acad. Sci. U.S.A. 83, 2407-2411, 1986
A:Title: Primary structure and cDNA cloning of human fibroblast collagenase inhibitor.
A:Reference number: A23534; MUID:86205964; PMID:3010309
A:Accession: A23534
A:Molecule type: mRNA
A:Residues: 1-207 <CAR>
A:Cross-references: UNIPARC:UPI00001135B1; GB:M12670; NID:9182482; PIDN:AA52436.1; PI
A:Note: Parts of this sequence were confirmed by protein sequencing
A:Note: carbohydrate binding sites were determined
R:Stricklin, G.P.; Welgus, H.G.
J. Biol. Chem. 269, 12252-12258, 1993
A:Title: Human skin fibroblast collagenase inhibitor.
A:Reference number: A20595; MUID:84032401; PMID:6313647
A:Accession: A20595
A:Molecule type: protein
A:Residues: 24-44, 'L', 46 <STR>
A:Cross-references: UNIPARC:UPI0000020C59D
A:Note: six disulfide bonds are present
R:Rapp, G.; Freudenstein, J.; Klaunder, J.; Mucha, J.; Wempe, F.; Zimmer, M.; Scheit, P
DNA Cell Biol. 9, 479-485, 1990
A:Title: Characterization of three abundant mRNAs from human ovarian granulosa cells.
A:Reference number: A35826; MUID:91025550; PMID:2171551
A:Accession: A35826
A:Molecule type: mRNA
A:Residues: 1-207 <RAP>
A:Cross-references: UNIPARC:UPI00001135B1; GB:M38188
R:Van Rans, M.; Norga, K.; Maure, S.; Proost, P.; Vandekerckhove, F.; Auwerx, J.; Van
Cytokine 3, 231-239, 1991

A>Title: The cytokine-protease connection: identification of a 96-kD THP-1 gelatinase an
A:Reference number: A48417; MUID:91355647; PMID:1653055
A:Accession: A48417
A:Molecule type: protein
A:Residues: 'X',25,'X',27-35,'X',37-52 <VAN>
A:Cross-references: UNIPARC:UPI0000173235
A:Experimental source: monocytic cell line THP-1
A>Note: sequence modified after extraction from NCBI backbone
A>Note: sequence incorrectly identified as 96k gelatinase
R:Osthus, A.; Knaemper, V.; Oberhoff, R.; Reinke, H.; Tschesche, H.
FEBS Lett. 296, 16-20, 1992
A>Title: Isolation and characterization of tissue inhibitors of metalloproteinases (TIMP
A:Reference number: S20318; MUID:9211176; PMID:1730286
A:Accession: S20318
A:Molecule type: protein
A:Residues: 'X',25,'X',27-35,'X',37-38 <OST>
A:Cross-references: UNIPARC:UPI0000173236
A:Experimental source: rheumatoid synovial fluid
R:Opdenaker, G.; Masure, S.; Proost, P.; Billiau, A.; van Damme, J.
FEBS Lett. 284, 73-78, 1991
A>Title: Natural human monocyte gelatinase and its inhibitor.
A:Reference number: S15872; MUID:91285112; PMID:1647974
A:Accession: S15872
A:Molecule type: protein
A:Residues: 'X',25,'X',27-35,'X',37-42,'X',44,'X',46,'X',48-51 <FEB>
A:Cross-references: UNIPARC:UPI0000173237
A:Experimental source: peripheral blood monocytes
R:Williamson, R.A.; Marston, F.A.O.; Angal, S.; Kokkalis, P.; Panico, M.; Morris, H.R.;
Blocham, J. 268, 267-274, 1990
A>Title: Disulphide bond assignment in human tissue inhibitor of metalloproteinases (TIMP
A:Reference number: A38978; MUID:90303199; PMID:2163605
A:Comment: annotation; disulfide bonds
R:Opbroek, A.; Kenney, M.C.; Brown, D.
Curr. Eye Res. 12, 877-883, 1993
A>Title: Characterization of a human corneal metalloproteinase inhibitor (TIMP-1).
A:Reference number: I52912; MUID:94123576; PMID:7507419
A:Accession: I52912
A:Molecule type: mRNA
A>Status: translated from GB/EMBL/DBJ
A:Residues: 1-207 <RES>
A:Cross-references: UNIPARC:UPI0000113581; GB:S68252; NID:G545022; PIDD:AAAD14009.1; PID:
R:Ritzdel, S.; Blaesser, U.; Gote, T.; Peitz, G.; Schuenen, E.; Schmitt, W.; Tschesche, H.
Eur. J. Biochem. 231, 714-719, 1995
A>Title: Evidence for the tissue inhibitor of metalloproteinases-1 (TIMP-1) in human pol
A:Reference number: S66461; MUID:95377303; PMID:7649172
A:Accession: S66461
A:Molecule type: protein
A:Residues: 24-38 <TRI>
A:Cross-references: UNIPARC:UPI0000173238
A:Experimental source: polymorphonuclear leukocytes
C:Comment: This protein, found in a variety of body fluids, complexes with metalloprotei
nase-specific, stimulating the growth and differentiation of only human and murine erythro
cytes. The remarkable heat stability of this protein may be due to disulfide bond fo
C:Genetic:
A:Gene: GDB:TIMP1; CLG1; TIMP
A:Cross-references: GDB:119615; OMIM:305370
A:Map position: Xp11.3-Xp11.23
C:Superfamily: metalloproteinase inhibitor
C:Keywords: erythropoiesis; glycoprotein; metalloproteinase inhibitor; mitogen
F1-23/Domain: signal sequence #status predicted <SIG>
F1-24-207/Product: metalloproteinase inhibitor 1 #status experimental <MAT>
F1-24-33,36-122,36-147,150-197,155-168,168-189/Disulfide bonds: #status experimental
F1-53,101/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 100.0%; Score 1124; DB 1; Length 207;
Best Local Similarity 100.0%; Pred. No. 1,5e-101;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFPEPLASGILLMLLWLPASRACVCPHPOTAFCSNDLVIRAKVGTPEVNOQTLLYOR 60
DB 1 MAFPEPLASGILLMLLWLPASRACVCPHPOTAFCSNDLVIRAKVGTPEVNOQTLLYOR 60

QY 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGFHRSHNSSEFLIAGKLQDGLLHTT 120

DB 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGFHRSHNSSEFLIAGKLQDGLLHTT 120
QY 121 TCSFVAPMNSLSLAQRGGTKTYTGCECTVFPCLSIIPCKLQSGTHCLMTDQLQSGSEK 180
DB 121 TCSFVAPMNSLSLAQRGGTKTYTGCECTVFPCLSIIPCKLQSGTHCLMTDQLQSGSEK 180
QY 181 GFQSHRLACLPREPGICTWQSLRSQIA 207
DB 181 GFQSHRLACLPREPGICTWQSLRSQIA 207

RESULT 2
JC4303
matrix metalloproteinase-1 tissue inhibitor - baboon
C:Species: Papio sp. (baboon)
C>Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 16-Jul-1999
C:Accession: JC4303
R:Forough, R.; Nikkari, S.T.; Hasenstab, D.; Lee, H.; Clowes, A.W.
Gene 163, 267-271, 1995
A>Title: Cloning and characterization of a cDNA encoding the baboon tissue inhibitor of
A:Reference number: JC4303; MUID:96011646; PMID:7590279
A:Accession: JC4303
A:Molecule type: mRNA
A:Residues: 1-207 <FOR>
A:Cross-references: UNIPARC:UPI000013658E; GB:L37295; NID:G561545; PIDD:AAA99943.1; PID:
A:Experimental source: smooth muscle cell
C:Comment: This protein, a member of the tissue inhibitor of matrix metalloproteinase fa
se and influences the proteinase activity. It has a role as a physiological molecule for
C:Genetic:
A:Gene: clmp-1
C:Superfamily: metalloproteinase inhibitor
C:Keywords: extracellular matrix; glycoprotein; metalloproteinase inhibitor
F1-53,101/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 99.4%; Score 1117; DB 2; Length 207;
Best Local Similarity 99.0%; Pred. No. 7.3e-101;
Matches 205; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFPEPLASGILLMLLWLPASRACVCPHPOTAFCSNDLVIRAKVGTPEVNOQTLLYOR 60
DB 1 MAFPEPLASGILLMLLWLPASRACVCPHPOTAFCSNDLVIRAKVGTPEVNOQTLLYOR 60

QY 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGFHRSHNSSEFLIAGKLQDGLLHTT 120
DB 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGFHRSHNSSEFLIAGKLQDGLLHTT 120

QY 121 TCSFVAPMNSLSLAQRGGTKTYTGCECTVFPCLSIIPCKLQSGTHCLMTDQLQSGSEK 180
DB 121 TCSFVAPMNSLSLAQRGGTKTYTGCECTVFPCLSIIPCKLQSGTHCLMTDQLQSGSEK 180

QY 181 GFQSHRLACLPREPGICTWQSLRSQIA 207
DB 181 GFQSHRLACLPREPGICTWQSLRSQIA 207

RESULT 3
A35685
metalloproteinase inhibitor 1 precursor - bovine
N:Alternate names: cartilage-derived neovascularization inhibitor; TIMP-1; tissue inhibi
tor; C:Species: Bos primigenius taurus (cattle)
C>Date: 21-Sep-1990 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C:Accession: A35685; B34468; B29712; A34833; 146979
R:Freundstein, J.; Wagner, S.; Luck, R.M.; Binspanner, R.; Schiele, K.H.
Biochem. Biophys. Res. Commun. 171, 250-256, 1990
A>Title: mRNA of bovine tissue inhibitor of metalloproteinase: sequence and expression
A:Reference number: A35685; MUID:90365711; PMID:2393392
A:Accession: A35685
A:Molecule type: mRNA
A:Residues: 1-207 <FRE>
A:Cross-references: UNIPROT:P20414; UNIPARC:UPI0000013658A; GB:M60073; NID:G163760; PIDD:
A:Experimental source: ovary cDNA library
R:De Clerck, Y.A.; Yean, T.D.; Ratzkin, B.J.; Lu, H.S.; Langley, K.E.

J. Biol. Chem. 264, 17445-17453, 1989
 A>Title: Purification and characterization of two related but distinct metalloproteinase
 A:Reference number: A34468; MUID:90008914; PMID:2551903
 A:Accession: B34468
 A:Molecule type: protein
 A:Residues: 24-52, 'X', 54-57, 'LY', 60-61, 'L', 63-65, 'L', 67-68, 'P' <DEC>
 A:Cross-references: UNIPARC:UPI0000173239
 A:Experimental source: culture medium of aortic endothelial cells
 R:Kaczorek, M.; Honore, N.; Ribes, V.; Denoux, P.; Cornet, P.; Cartwright, T.; Strecek, B.; Technology 5, 595-598, 1987
 A>Title: Molecular cloning and synthesis of biologically active human tissue inhibitor
 A:Reference number: A29712
 A:Accession: B29712
 A:Molecule type: protein
 A:Residues: 24-37 <KAC>
 A:Cross-references: UNIPARC:UPI000017323A
 A:Experimental source: culture medium of fibroblastic BC 21 cells
 A>Note: protein inhibits angiogenesis
 R:Moses, M.A.; Sudhalter, J.; Langer, R.
 Science 248, 1408-1410, 1990
 A>Title: Identification of an inhibitor of neovascularization from cartilage.
 A:Reference number: A34833; MUID:90288433; PMID:1694043
 A:Accession: A34833
 A:Molecule type: protein
 A:Residues: 24-51 <MOS>
 A:Cross-references: UNIPARC:UPI000017323B
 A:Experimental source: cartilage
 R:Sato, T.; Kobayashi, K.; Yamashita, S.; Kikuchi, M.; Sendai, Y.; Hoshi, H.
 Biol. Reprod. 50, 835-844, 1994
 A>Title: Tissue inhibitor of metalloproteinases (TIMP-1) produced by granulosa and oviduct
 A:Reference number: 146979; MUID:94257757; PMID:8199264
 A:Accession: 146979
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-207 <SAT>
 A:Cross-references: UNIPARC:UPI0000136F8A; GB:S70841; NID:9546973; PIDN:AB30892.1; PID:
 A:Function:
 A>Description: regulation of extracellular matrix remodeling by inhibition of matrix metalloproteinases
 A>Note: transcription induced by cytokines, tumor promoters, and anti-inflammatory agent
 A>Note: TIMP-1 and TIMP-3 have distinct but overlapping tissue-specific expression pattern
 C:Keywords: erythropoiesis; extracellular matrix; glycoprotein; metalloproteinase inhibitor
 F:1-207/Product: metalloproteinase inhibitor 1 #status experimental <MAR>
 F:24-93/26-122-36-147-150-157-155-160-168-189/Divalent bonds: #status predicted
 F:53-101/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 88.5%; Score 995; DB 1; Length 207;
 Best Local Similarity 87.0%; Pred. No. 5e-89;
 Matches 180; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

QY 1 MAPEPLASGILLMLIAPSRACVPPHQTAFNCNSDLVIRAKFVGTEPVNOQTLYOR 60
 Db 1 MAPAPMASGILLMLIAPSRACVPPHQTAFNCNSDLVIRAKFVGTEPVNOQTLYOR 60
 QY 61 YEIMTMYKGFQALGDAADIRFYTPPAMESVCGYFHRSHNRSEFLIAGLQDGLHIT 120
 Db 61 YEIMTMYKGFQALGDAADIRFYTPPAMESVCGYFHRSHNRSEFLIAGLQDGLHIT 120
 QY 121 TCSFVAPWNSISLQORGFRTKYTVGCECTVPFCLSPCKLQSGTHCLMTDQLTGSSEK 180
 Db 121 TCSFVAPWNSISLQORGFRTKYTVGCECTVPFCLSPCKLQSGTHCLMTDQLTGSSEK 180
 QY 121 TCSFVAPWNSISLQORGFRTKYTVGCECTVPFCLSPCKLQSGTHCLMTDQLTGSSEK 180
 Db 121 TCSFVAPWNSISLQORGFRTKYTVGCECTVPFCLSPCKLQSGTHCLMTDQLTGSSEK 180
 QY 181 GFQSRHLACLPRPBGCLTQWSLRQIA 207
 Db 181 GFQSRHLACLPRPBGCLTQWSLRQIA 207

RESULT 4
 147061
 collagenase inhibitor - pig
 C:Species: Sus scrofa domestica (domestic pig)

C>Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004
 C:Accession: 147061
 R:Tanaka, T.; Andon, N.; Takeya, T.; Sato, E.
 Mol. Cell. Endocrinol. 83, 65-71, 1992
 A>Title: Differential screening of ovarian cDNA libraries detected the expression of t
 A:Reference number: 147061; MUID:92201478; PMID:1312961
 A:Accession: 147061
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-207 <TAN>
 A:Cross-references: UNIPARC:UPI000016C64A; GB:S96211; NID:9247729; PID:
 C:Superfamily: metalloproteinase inhibitor

Query Match 86.4%; Score 971; DB 2; Length 207;
 Best Local Similarity 84.1%; Pred. No. 1.1e-86;
 Matches 174; Conservative 14; Mismatches 19; Indels 0; Gaps 0;

QY 1 MAPEPLASGILLMLIAPSRACVPPHQTAFNCNSDLVIRAKFVGTEPVNOQTLYOR 60
 Db 1 MSPAPMASGILLMLIAPSRACVPPHQTAFNCNSDLVIRAKFVGTEPVNOQTLYOR 60
 QY 61 YEIMTMYKGFQALGDAADIRFYTPPAMESVCGYFHRSHNRSEFLIAGLQDGLHIT 120
 Db 61 YEIMTMYKGFQALGDAADIRFYTPPAMESVCGYFHRSHNRSEFLIAGLQDGLHIT 120
 QY 121 TCSFVAPWNSISLQORGFRTKYTVGCECTVPFCLSPCKLQSGTHCLMTDQLTGSSEK 180
 Db 121 TCSFVAPWNSISLQORGFRTKYTVGCECTVPFCLSPCKLQSGTHCLMTDQLTGSSEK 180
 QY 121 TCSFVAPWNSISLQORGFRTKYTVGCECTVPFCLSPCKLQSGTHCLMTDQLTGSSEK 180
 Db 121 TCSFVAPWNSISLQORGFRTKYTVGCECTVPFCLSPCKLQSGTHCLMTDQLTGSSEK 180
 QY 181 GFQSRHLACLPRPBGCLTQWSLRQIA 207
 Db 181 GFQSRHLACLPRPBGCLTQWSLRQIA 207

RESULT 5
 146964
 metalloproteinase tissue inhibitor 1 precursor [similarity] - sheep
 C:Species: Ovis orientalis aries, Ovis aries (domestic sheep)
 C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
 C:Accession: 146964
 R:Smith, G.W.; Goetz, T.L.; Anthony, R.V.; Smith, M.F.
 Endocrinology 134, 344-352, 1994
 A>Title: Molecular cloning of an ovine ovarian tissue inhibitor of metalloproteinases
 A:Reference number: 146964; MUID:94102210; PMID:8275949
 A:Accession: 146964
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-207 <SMI>
 A:Cross-references: UNIPARC:UPI0000136F92; GB:S67450; NID:9456989; PID:
 C:Superfamily: metalloproteinase inhibitor

Query Match 85.5%; Score 961; DB 2; Length 207;
 Best Local Similarity 85.7%; Pred. No. 9.8e-86;
 Matches 174; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

QY 1 MAPEPLASGILLMLIAPSRACVPPHQTAFNCNSDLVIRAKFVGTEPVNOQTLYOR 60
 Db 1 MAPAPMASGILLMLIAPSRACVPPHQTAFNCNSDLVIRAKFVGTEPVNOQTLYOR 60
 QY 61 YEIMTMYKGFQALGDAADIRFYTPPAMESVCGYFHRSHNRSEFLIAGLQDGLHIT 120
 Db 61 YEIMTMYKGFQALGDAADIRFYTPPAMESVCGYFHRSHNRSEFLIAGLQDGLHIT 120
 QY 121 TCSFVAPWNSISLQORGFRTKYTVGCECTVPFCLSPCKLQSGTHCLMTDQLTGSSEK 180
 Db 121 TCSFVAPWNSISLQORGFRTKYTVGCECTVPFCLSPCKLQSGTHCLMTDQLTGSSEK 180
 QY 121 TCSFVAPWNSISLQORGFRTKYTVGCECTVPFCLSPCKLQSGTHCLMTDQLTGSSEK 180
 Db 121 TCSFVAPWNSISLQORGFRTKYTVGCECTVPFCLSPCKLQSGTHCLMTDQLTGSSEK 180
 QY 181 GFQSRHLACLPRPBGCLTQWSLR 203
 Db 181 GFQSRHLACLPRPBGCLTQWSLR 203

RESULT 6
A3350 metalloproteinase inhibitor 1 precursor - rabbit
N:Alternate names: TIMP-1; tissue inhibitor of metalloproteinases 1
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 30-Jun-1992 #sequence_revision 12-Apr-1996 #ext_change 09-Jul-2004
A:Accession: A33350; A30864
R:Horowitz, S.; Dafni, N.; Shapiro, D.L.; Holm, B.A.; Notter, R.H.; Quible, D.J.
J: Biol. Chem. 264, 7092-7095, 1989
A:Title: Hyperoxic exposure alters gene expression in the lung. Induction of the tissue
A:Reference number: A33350; MUID:89214135; PMID:2708356
A:Accession: A33350
A:Molecule type: mRNA
A:Residues: 1-206 <HOR>
A:Cross-references: UNIPROT:P20614; UNIPARC:UPI0000136F90; GB:J04712; NID:9165742; PIDN:
A:Experimental source: hyperoxi-exposed lung of New Zealand White rabbits
C:Comment: Expression of this protein in the lung is induced 6-fold by hyperoxia.
C:Function:
A:Description: regulation of extracellular matrix remodeling by inhibition of matrix met
possibly controlling their activation; TIMP-1 and TIMP-2 possess erythroid potentiating
A>Note: transcription induced by cytokines, tumor promoters, and anti-inflammatory agent
A>Note: TIMP-1 and TIMP-3 have distinct but overlapping tissue-specific expression patte
C:Superfamily: metalloproteinase inhibitor
C:Keywords: erythropoiesis; extracellular matrix; glycoprotein; metalloproteinase inhibi
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-206/Product: metalloproteinase inhibitor 1 #status predicted <MAT>
F:24-93-26-122-36-147-150-196-155-160-168-188-189/Disulfide bonds: #status predicted
F:53-101/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 80.3%; Score 902.5; DB 1; Length 206;
Best Local Similarity 80.8%; Pred. No. 4.6e-80;
Matches 164; Conservative 13; Mismatches 25; Indels 1; Gaps 1;

QY 1 MAPPEPLASGILLMLLPLASRACVPPHPPTACNSDLVIRAFVGTPEVNOGTLTYR 60
DB 1 MAPPLAASSMILLMLLPLASRACVPPHPPTACNSDLVIRAFVGTPEVNOGTLTYR 60
QY 61 YEIKMTKMKGFQALGDADIRFVYTPAMESVCGYFHRSHNSSEFLIAGKLODGLHTT 120
DB 61 YEIKTKMKKGFQALGDADIRFVYTPAMESVCGYFHRSHNSSEFLIAGKLODGLHTT 120
QY 121 TCSFVAPMNSLSLAQRGFTKTYTVGCECTVPCLSIPTCKLQSGTHCLMTDQLQSGSEK 180
DB 121 TCSFVAPMNSLSFSGQSGFTKTYTVAGCDMCTVACASIPCHLESPTHCLMTDSSL-GSDK 179
QY 181 GFOSRHACLPRPGLCTWOSLR 203
DB 180 GFOSRHACLPRPGLCAMESLR 202

RESULT 7
A26106 metalloproteinase inhibitor 1 precursor - mouse
N:Alternate names: erythroid potentiating activity (EPA); fibroblast collagenase inhibit
C:Species: Mus musculus (house mouse)
C>Date: 05-Oct-1988 #sequence_revision 12-Apr-1996 #ext_change 09-Jul-2004
A:Accession: A26917; A26106; A26633; A05276
R:Johnson, M.D.; Housey, G.M.; Kirschmeier, P.T.; Weinstein, I.B.
Mol. Cell. Biol. 7, 2821-2829, 1987
A:Title: Molecular cloning of gene sequences regulated by tumor promoters and mitogens
A:Reference number: A26917; MUID:88038821; PMID:3670294
A:Accession: A26917
A:Molecule type: mRNA
A:Residues: 1-205 <JOH>
A:Cross-references: UNIPROT:P12032; UNIPARC:UPI00000018BB; GB:M17243; NID:9202111; PIDN:
A:Experimental source: embryonic fibroblast cDNA library
R:Edwards, D.R.; Waterhouse, P.; Holman, M.L.; Denhardt, D.T.
Nucleic Acids Res. 14, 8863-8878, 1986
A:Title: A growth-responsive gene (16C8) in normal mouse fibroblasts homologous to a hum
p18.
A:Reference number: A26106; MUID:87066763; PMID:3024122
A:Accession: A26106
A:Molecule type: mRNA

A:Residues: 1-205 <EDM>
A:Cross-references: UNIPARC:UPI00000018BB; GB:X04684; NID:949702; PIDN:CAA28387.1; PID
A:Experimental source: embryonic fibroblast cDNA library
R:Gewert, D.R.; Coulombe, B.; Castelfino, M.; Skup, D.; Williams, B.R.G.
EMBO J. 6, 651-657, 1987
A:Title: Characterization and expression of a murine gene homologous to human EPA/TIMP
A:Reference number: A26633; MUID:87218524; PMID:3034603
A:Accession: A26633
A:Molecule type: DNA
A:Residues: 1-51, 'R', 53-66, 'M', 67-116, 'KF', 119-120, 'N', 122-138, 'V', 140-142, 'KN', 144-193
A:Cross-references: UNIPARC:UPI000016394C; GB:M28312; NID:9193040; PIDN:AA842179.1, PLE
R:Skup, D.; Windass, J.D.; Sor, F.; George, H.; Williams, B.R.G.; Fukushima, H.; De Maey
Nucleic Acids Res. 10, 3069-3084, 1982
A:Title: Molecular cloning of partial cDNA copies of two distinct mouse IFN-beta mRNAs
A:Reference number: A93424; MUID:82247191; PMID:6179042
A:Accession: A05276
A:Molecule type: mRNA
A:Residues: 168-193, 'L', 195-205 <SKU>
A:Cross-references: UNIPARC:UPI00000E8041; GB:V00755; GB:J00425; NID:951554; PIDN:CAA24
A:Note: authors thought this clone represented a form of interferon beta
C:Genetics:
A:Gene: Timp
A:Map position: X
A:Introns: 41/3; 68/3; 110/3; 152/3
C:Function:
A:Description: regulation of extracellular matrix remodeling by inhibition of matrix me
possibly controlling their activation; TIMP-1 and TIMP-2 possess erythroid potentiatin
A>Note: transcription induced by cytokines, tumor promoters, and anti-inflammatory agen
A>Note: TIMP-1 and TIMP-3 have distinct but overlapping tissue-specific expression pat-
C:Superfamily: metalloproteinase inhibitor
C:Keywords: erythropoiesis; extracellular matrix; glycoprotein; metalloproteinase inhibi
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-205/Product: metalloproteinase inhibitor 1 #status predicted <MAT>
F:25-24-27-123-37-148-151-197-156-161-169-189/Disulfide bonds: #status predicted
F:54-102/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 74.5%; Score 837.5; DB 1; Length 205;
Best Local Similarity 74.3%; Pred. No. 9.2e-74;
Matches 150; Conservative 26; Mismatches 25; Indels 1; Gaps 1;

QY 1 MAPPEPLASGILLMLLPLASRACVPPHPPTACNSDLVIRAFVGTPEVNOGTLTYR 60
DB 2 MAPFASLASGILLMLLPLASRACVPPHPPTACNSDLVIRAFVGTPEVNOGTLTYR 61
QY 61 YEIKMTKMKGFQALGDADIRFVYTPAMESVCGYFHRSHNSSEFLIAGKLODGLHTT 120
DB 62 YEIKMTKMKGFQALGDADIRFVYTPAMESVCGYFHRSHNSSEFLIAGKLODGLHTT 121
QY 121 TCSFVAPMNSLSLAQRGFTKTYTVGCECTVPCLSIPTCKLQSGTHCLMTDQLQSGSEK 180
DB 122 ACSFVAPMNTLSPAQGRFSTKYSAGCGVCTVPCLSIPTCKLESPTHCLMTDQVLVGSF- 180
QY 181 GFOSRHACLPRPGLCTWOSLR 202
DB 181 DYOSRHACLPRPGLCTWOSLR 202

RESULT 8
JC2557 metalloproteinase inhibitor 1 precursor - rat
N:Alternate names: TIMP-1
C:Species: Rattus norvegicus (Norway rat)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #ext_change 09-Jul-2004
A:Accession: JC2557; B39120; S20326
R:Okada, A.; Garnier, J.M.; Vicaire, S.; Bassez, P.
Gene 147, 301-302, 1994
A:Title: Cloning of the cDNA encoding rat tissue inhibitor of metalloproteinase 1 (TIMP-
A:Reference number: JC2557; MUID:95011636; PMID:7926820
A:Accession: JC2557
A:Molecule type: mRNA
A:Residues: 1-217 <OKA>
A:Cross-references: UNIPROT:P30120; UNIPARC:UPI0000136F91; EMBL:U06179; NID:9468057; PID

Wed Apr 12 09:54:35 2006

R.Olson Jr., J.A.; Shiverick, K.T.; Ogilvie, S.; Buhl, W.C.; Raizada, M.K.
 Proc. Natl. Acad. Sci. U.S.A. 88, 1928-1932, 1991
 A:Title: Angiotensin II induces secretion of plasminogen activator inhibitor 1 and a tis
 A:Reference number: A39120; MUID:91156719; PMID:2000398
 A:Accession: B39120
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 24-36, 'B', '38', 'B', '40-42', 'X', '44' <OLS>
 A:Cross-references: UNIPARC:UPI000017323C
 R.Roswit, W.T.; McCourt, D.W.; Partidge, N.C.; Jeffrey, J.J.
 Arch. Biochem. Biophys. 292, 402-410, 1992
 A:Title: Purification and sequence analysis of two rat tissue inhibitors of metalloprote
 A:Reference number: S20325; MUID:92117648; PMID:1309971
 A:Accession: S20326
 A:Molecule type: protein
 A:Residues: 24-45 <ROS>
 A:Cross-references: UNIPARC:UPI000017323D
 C:Function:
 A:Description: regulation of extracellular matrix remodeling by inhibition of matrix met
 possibly controlling their activation: TIMP-1 and TIMP-2 possess erythroid potentiating
 A:Note: transcription induced by cytokines, tumor promoters, and anti-inflammatory agent
 A:Note: TIMP-1 and TIMP-3 have distinct but overlapping tissue-specific expression patte
 C:Superfamily: metalloproteinase inhibitor
 C:Keywords: erythropoiesis; extracellular matrix; glycoprotein; metalloproteinase inhibi
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-217/Product: metalloproteinase inhibitor 1 #status experimental <MAT>
 F:101,130/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 72.8%; Score 818; DB 1; Length 217;
 Best Local Similarity 72.3%; Pred. No. 7.7e-72;
 Matches 146; Conservative 24; Mismatches 32; Indels 0; Gaps 0;

QY 1 MAPEPLASGLILMLIAPSRACVPPHPTAFNCSDIVIRAFVGTPEVNOITLYOR 60
 DB 1 MAPPLASGLILMLIASSKACSCAPTHPTAFNCSDIVIRAFVGTPEVNOITLYOR 60
 QY 61 YEIMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHRSEFLIAGKLDGLHIT 120
 DB 61 YEIMTKMLKGFDAVGNATGRFATTPAMESICGVYHKSQNRSEFLIAGKLRNGLHIT 120
 QY 121 TCSFVAPWNSLSLAQRGFTTYTVGCECTVPPCLSIIPCKLQSGTHCLMTDQLQSGEK 180
 DB 121 ACSFLVPWHLSPAQOKAFVKTYSAGCGVCTVPCSAIPCKLESDSHCLMTDQLMGSEK 180
 QY 181 GFOSRHACLPREPGLCTWQSL 202
 DB 181 GYQSDHFACLPRNPDLCTWQYL 202

RESULT 9

JH0683
 metalloproteinase inhibitor 2 precursor - mouse
 N:Alternate names: TIMP-2; tissue inhibitor of metalloproteinases 2
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: JH0683; JCI234; S18428; S15987; S26189
 R:Shimizu, S.; Malik, K.; Sejima, H.; Kishi, J.; Hayakawa, T.; Koiwai, O.
 Gene 114, 291-292, 1992
 A:Title: Cloning and sequencing of the cDNA encoding a mouse tissue inhibitor of metallo
 A:Reference number: JH0683; MUID:92290292; PMID:1601312
 A:Accession: JH0683
 A:Molecule type: mRNA
 A:Residues: 1-220 <SHI>
 A:Cross-references: UNIPROT:P25785; UNIPARC:UPI00000278E8; EMBL:X62622; NID:954801; PIDN
 R:Lecco, K.J.; Hayden, L.J.; Sharma, R.R.; Rocheleau, H.; Greenberg, A.H.; Edwards, D.R.
 Gene 117, 209-217, 1992
 A:Title: Differential regulation of TIMP-1 and TIMP-2 mRNA expression in normal and Ha-4
 A:Reference number: JCI234; MUID:92347695; PMID:1639268
 A:Accession: JCI234
 A:Molecule type: mRNA
 A:Residues: 1-11, 'H', '13-20', 'L', '22-194', 'E', '196-220' <DEC>
 A:Cross-references: UNIPARC:UPI000016D07D; GB:M33954; NID:9202053; PIDN:AAA40446.1; PID:

R.Kishi, J.
 Matrix 11, 373, 1991
 A:Title: Correction.
 A:Reference number: S18428; MUID:92244125; PMID:1667327
 A:Accession: S18428
 A:Molecule type: protein
 A:Residues: 27-46, 'H', '48, 50-53', 'VD', '56', 'DY', 'KIS'
 A:Cross-references: UNIPARC:UPI0000173246
 R.Kishi, J.I.; Ogawa, K.; Yamamoto, S.; Hayakawa, T.
 Matrix 11, 10-16, 1991
 A:Title: Purification and characterization of a new tissue inhibitor of metalloprotein
 A:Reference number: S15987; MUID:91226375; PMID:1851244
 A:Accession: S15987
 A:Molecule type: protein
 A:Residues: 27-46, 'HLK', '50-52', 'LX', '55-56', 'DXK', '60', 'X', '62' <K12>
 A:Cross-references: UNIPARC:UPI0000173247
 A:Note: this sequence has been revised in reference S18428
 C:Function:
 A:Description: regulation of extracellular matrix remodeling by inhibition of matrix m
 possibly controlling their activation: TIMP-1 and TIMP-2 possess erythroid potentiati
 C:Superfamily: metalloproteinase inhibitor
 C:Keywords: erythropoiesis; extracellular matrix; metalloproteinase inhibitor; mitogen
 F:1-26/Domain: signal sequence #status predicted <SIG>
 F:27-220/Product: metalloproteinase inhibitor 2 #status experimental <MAT>
 F:27-98,29-127,39-152,154-201,159-164,172-193/Disulfide bonds: #status predicted

Query Match 37.4%; Score 420.5; DB 1; Length 220;
 Best Local Similarity 42.8%; Pred. No. 2.8e-33;
 Matches 86; Conservative 30; Mismatches 70; Indels 15; Gaps 6;

QY 7 LASGILLMLIAPSRACVPPHPTAFNCSDIVIRAFVGTPEVNO-TTLYO----- 59
 DB 10 LALGILLASLVRPADSCSPVHPQAFNCADVIRAKAVSEKVDGNDIYGNPIKRI 69
 QY 60 RYRKMTMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHRSEFLIAGKLDGLH 118
 DB 70 QYEIKQIMPR-----GPDKQIEFTYTPASSAVCG-VSLDVGCKKEYIILAKABEDGMH 123
 QY 119 ITTCSFVAPWNSLSLAQRGFTTYTVGCECTVPPCLSIIPCKLQSGTHCLMTDQLQGS 178
 DB 124 ITLCDFIWMDLTLLITQKSLNHRYQMG-ECKITRCWIPICYSIPDECLMMDVWTERK 182
 QY 179 EKGFSRHACLPREPGLCTW 199
 DB 183 INGHQAFPCIKRSDSCAW 203

RESULT 10

153415
 tissue inhibitor of metalloproteinase type 2 - rat
 C:Species: Rattus sp. (rat)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999
 C:Accession: 153415
 R:Sanctoro, M.; Battaglia, C.; Zhang, L.; Carlomagno, F.; Martelli, M.L.; Salvatore, D.
 Exp. Cell Res. 213, 398-403, 1994
 A:Title: Cloning of the rat tissue inhibitor of metalloproteinases type 2 (TIMP-2) ge
 A:Reference number: 153415; MUID:94326839; PMID:8050496
 A:Accession: 153415
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-220 <RES>
 A:Cross-references: UNIPARC:UPI00000102A; GB:S72594; NID:9619232; PIDN:AAC60687.1; P:
 C:Genetics:
 A:Gene: TIMP-2
 C:Superfamily: metalloproteinase inhibitor
 Query Match 37.4%; Score 420.5; DB 2; Length 220;
 Best Local Similarity 42.8%; Pred. No. 2.8e-33;
 Matches 86; Conservative 30; Mismatches 70; Indels 15; Gaps 6;

QY 7 LASGILLMLIAPSRACVPPHPTAFNCSDIVIRAFVGTPEVNO-TTLYO----- 59
 DB 10 LALGILLATLVRPADSCSPVHPQAFNCADVIRAKAVSEKVDGNDIYGNPIKRI 69

Rooba, Y.; Goto, Y.; Kimura, Y.; Suzuki, F.; Hise, T.; Takahashi, K.; Takigawa, M.
Biochim. Biophys. Acta 1245, 1-8, 1995
A>Title: Purification of an angiogenesis inhibitor from culture medium conditioned by a
A:Accession: S58794
A:Release: S58794
A:Status: preliminary
A:Molecule type: protein
A:Residues: 27-37 <OH>
A:Cross-references: UNIPARC:UPI0000173245
C:GeneticS:
A:Gene: GDB:TIMP2
A:Cross-references: GDB:132612; OMIM:188825
A:Map position: 17q25-17q25
C:Function:
A:Description: regulation of extracellular matrix remodeling by inhibition of matrix met-
possibly controlling their activation; TIMP-1 and TIMP-2 possess erythroid potentiating
C:Superfamily: metalloproteinase inhibitor
C:Keywords: erythropoiesis; extracellular matrix; metalloproteinase inhibitor; mtogen
F1:1-26/domain: signal sequence #status predicted <SIG>
F127-220/Product: metalloproteinase inhibitor 2 #status experimental <MAT>
F127-98, 29-127, 39-152, 154-201, 159-164, 172-193/Disulfide bonds: #status predicted
F127-98, 29-127, 39-152, 154-201, 159-164, 172-193/Disulfide bonds: #status predicted

Query Match 37.0%; Score 415.5; DB 1; Length 220;
Best Local Similarity 42.3%; Pred. No. 8.4e-33;
Matches 85; Conservative 30; Mismatches 71; Indels 15; Gaps 6;

QY 7 LASGILLMLTLPAPRACCTVPPHPOTACNSGDLVTRAFVGVPEVNO---TTLQ----- 59
 Db 10 LALGILLTLTLRPADGSCSPVHPQACNADVIRAAVSKSEYVDSGNDIYGNIYKAI 69
 QY 60 RYEIRMTYKYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEELIAGKLQ-DGLAH 118
 Db 70 QYEIKQIIMFK-----GPEKDIIEFIYTAPSAVCG-VSLDVGGKKYLLIAGRAEGGGRKH 123
 QY 119 ITTCSFVAPWNSLSLAQRGRGTYTYTVGCECTVFPCLSI PCKLQSGTHCLMTDQLQGS 178
 Db 124 ITLCFIPVMDTLSTQKKSLNHRVQMG-C-ECKITRCPMIPCYISSPDECLMMDVTEKN 182
 QY 179 EKGFSRHLACLPRRGLCTW 199
 Db 183 INGHQAKFPACIKRSDGSCAW 203

RESULT 13

metalloproteinase inhibitor 2 precursor - bovine
N:Alternate names: collagenase inhibitor, tissue inhibitor of metalloproteinases (TIMP-2)
C:Species: Bos primigenius taurus (cattle)
C:/Date: 16-Nov-1990 #sequence revision 12-Apr-1996 #text_change 09-Jul-2004
C:/Accession: A35996; A34468; A25322; S28151
R:Boone, T.C.; Johnson, M.J.; De Clerck, Y.A.; Langley, K.E.
Proc. Natl. Acad. Sci. U.S.A. 87, 2800-2804, 1990
A:/Title: cDNA cloning and expression of a metalloproteinase inhibitor related to tissue
A:/Reference number: A35996; MUID:90207285; PMID:2157214
A:/Accession: A35996
A:/Molecule type: mRNA
A:/Residues: 1-720 <BOO>
A:/Cross-references: UNIPROT:P16368; UNIPARC:UP10000136F93; GB:M32303; NID:G163341; PIDN:
A:/Experimental source: aortic endothelial cDNA library
R:De Clerck, Y.A.; Yeann, T.D.; Ratckin, B.J.; Lu, H.S.; Langley, K.E.
J. Biol. Chem. 264, 17445-17453, 1989
A:/Title: Purification and characterization of two related but distinct metalloproteinases
A:/Reference number: A34468; MUID:9008914; PMID:2551903
A:/Accession: A34468
A:/Molecule type: Protein
A:/Residues: 27-71 <DEC>
A:/Cross-references: UNIPARC:UP1000017324A
A:/Experimental source: culture medium of aortic endothelial cells
R:Murray, J.B.; Allison, K.; Stuhalter, J.; Langer, R.
J. Biol. Chem. 261, 4154-4159, 1986
A:/Title: Purification and partial amino acid sequence of a bovine cartilage-derived collagen
A:/Reference number: A25322; MUID:86140235; PMID:3005321
A:/Accession: A25322

A: Molecule type: protein
A: Residues: 27-41, 'C', 43-55, 'EX', 58-59, 'X', 61-66, 'XS', 69-71 <MUR>
A: Cross-References: UNIPARC:UPI000017324B
A: Experimental source: cartilage
R: DeClerck, Y.A., Yean, T.D., Lee, Y., Tomich, J.M., Langley, K.E.
Biochem. J. 289, 65-69, 1993
A: Title: Characterization of the functional domain of tissue inhibitor of metalloproteinase
A: Reference number: S28151, MUID:93143691, PMID:8424773
A: Contents: annotation; functional domain
C: Function:
A: Description: regulation of extracellular matrix remodeling by inhibition of matrix metalloproteinase
possibly controlling their activation; TIMP-1 and TIMP-2 possess erythroid potentiating activity
C: Superfamily: metalloproteinase inhibitor
C: Keywords: erythropoiesis; extracellular matrix; metalloproteinase inhibitor; mitogen
F/1-56/Domain: signal sequence #status predicted <SIG>
F/27-220/Product: metalloproteinase inhibitor 2 #status predicted <MAT>
F/27-98, 29-127, 39-152, 154-201, 159-164, 172-193/Disulfide bonds: #status predicted

Query Match 35.1%; Score 394.5; DB 1; Length 220;
Best Local Similarity 41.1%; Pred. No. 9.1e-31;
Matches 83; Conservative 31; Mismatches 73; Indels 15; Gaps 6;

QY 6 LAGSILLMLLWLPASRACITCVPHAPOTAFCSNLSLVI RAKVGRPEVWQ-ITLWQ----- 59
 Db 9 PLAFCLLLGLTLLPPADSCSPVHPQAFENADIVIRAKAVNKEEVDGSCNDITGNPIKR 68
 QY 60 -RYEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNRSEBELLIGKLQ-DGLL 117
 Db 69 IQYELKQIKMK-----GPDQDIEFIYTPAPAAVCG-VSLDIGRKEVLLINGKAEKGNQM 122
 QY 118 HITTCSPVAPNNSLSLQNRGFTYTVGSECEVTFPCLSLIPCKLQSGTHCLMTDQLIG 177
 Db 123 HITLCDFIVPDWTLSATQKKSINRHYQMG-C-ECKITRCMIPCYISSPDECECLMDWVTEK 181
 QY 178 SEKGFSQSHLACLPRBGLCTW 199
 Db 182 NINHQAKFFACIKRSDGSCAW 203

RESULT 14

metalloproteinase inhibitor 3 precursor [validated] - human
 N:Alternate names: mlg-5 protein; TIMP-3; tissue inhibitor of metalloproteinases 3
 C:Species: Homo sapiens (man)
 C:Date: 06-Jan-1995 #sequence revision 12-Apr-1996 #text change 09-Jul-2004
 C:Accession: S45317, S59515, S53870, I380823, A49614, C56937, I53025, S47041
 R:Urita, J.A.; Ferrando, A.A.; Velasco, G.; Freije, J.M.P.; Lopez-Otin, C.
 Cancer Res. 54, 2091-2094, 1994
 A>Title: Structure and expression in breast tumors of human TIMP-3, a new member of the
 A:Reference number: S45317; MUID:94228524; PMID:8174111
 A:Accession: S45317
 A:Molecule type: mRNA
 A:Residues: 1-211 <UK1>
 A:Cross-references: UNIPROT:P35625; UNIPARC:UPI000005F30A; EMBL:X76227; NID:g495251; PI
 A:Experimental source: breast tumor cDNA library
 R:Siibiger, S.M.; Jacobsen, V.L.; Cupples, R.L.; Koski, R.A.
 Gene 141, 293-297, 1994
 A>Title: Cloning of cDNA encoding human TIMP-3, a novel member of the tissue inhibitor
 A:Reference number: S59515; MUID:94215920; PMID:8163205
 A:Accession: S59515
 A:Molecule type: mRNA
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-211 <SL1>
 A:Cross-references: UNIPARC:UPI000005F30A; EMBL:U02571; NID:g472309; PIDD:AAA17672.1; P
 R:Kishnani, N.S.; Staackus, P.W.; Yang, T.T.; Masiarz, F.R.; Hawkes, S.P.
 Matrix Biol. 14, 479-488, 1994
 A>Title: Identification and characterization of human tissue inhibitor of metalloprotein
 A:Reference number: S53870
 A:Accession: S53870
 A:Molecule type: protein
 A:Residues: 'X',25,'XX',28,'X',30-35,'X',37,'X',39-41 <K1S>
 A:Cross-references: UNIPARC:UPI000017324C
 R:Wick, M.; Burger C.; Brunesbach, S.; Lucibello, F.C.; Mueller, R.

[illegible]

```
C|Species: Criticellus longicaudatus (long-tailed hamster)
C|Date: 06-Jan-1995 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C|Accession: S38624
R|Suzuki, Y.
submitted to the EMBL Data Library, November 1993
A|Reference number: S38624
A|Accession: S38624
A|Molecule type: mRNA
A|Residues: 1-196 <SUZ>
A|Cross-references: UNIPROT:Q60453; UNIPARC:UPI0000136F97; EMBL:X75924; MID:G414876; PDB:
C|Function:
A|Description: regulation of extracellular matrix remodeling by inhibition of matrix metalloproteinase inhibitor
possibly controlling their activation; TIMP-1 and TIMP-2 possess erythrold potentiating
C|Keywords: metalloproteinase inhibitor
C|Keywords: erythropoiesis; extracellular matrix; metalloproteinase inhibitor; mitogen
F,3-74,5-103,15-128,130-177,135-140,148-169/Distulfide bonds: #stratue predicted
F,3-74,5-103,15-128,130-177,135-140,148-169/Distulfide bonds: #stratue predicted

Query Match      34.6%; Score 388.5; DB 1; Length 196;
Best Local Similarity 42.5%; Pred. No. 3.1e-30;
Matches 79; Conservative 26; Mismatches 66; Indels 15; Gaps 6;

QY 22 RACCTVPHHOTACNSDLVIRAKFVGTPRPVNQ-TTLXQ-----RYEIKTKIMYGKFGQA 74
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 1 RACCSFVHPPOARCNADVIRAKAVSEKVDSCNDNYGNPIRIOTIEIQTIMFK--- 56
   |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||

QY 75 LGADADIRFYVTAPMBSVCGYFFHRSHNRSEEFILAGLKQ-DGLHLITTCSFVAWMSLSL 133
   ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 57 -GPKDIEFIITYTAASSAVCG-VSLDVGKKKEYLIIAGAEBDGMHITLCOFIYPMDTIST 114
   ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY 134 AQRNGFTKYTVSEECTVFPPCUSIPCKLOSCHCLMTDOLLQGSEKGFOFSRLACLPRE 193
   ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 115 TQKSJLNHRXYOMCG-ECKITRCPMIPCYSBPBECIMMDVTEKISINGOAKFEFACIKRS 173
   ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY 194 PGLCTW 199
   |||||
Db 174 DGSGAW 179
```

Search completed: April 10, 2006, 18:07:32
Job time : 13.8416 secs

RESULT 15
S38624
metalloproteinase inhibitor 2 precursor - long-tailed hamster (fragment)
N/Alternate names: TIMP-2; tissue inhibitor of metalloproteinases 2

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 10, 2006, 17:55:05 ; Search time 79.703 Seconds

(without alignments)
1141.129 Million cell updates/sec

Title: US-10-734-564-100

Perfect score: 1124
Sequence: 1 MAPPEPLASGILLMLAP.....ACLPREPLCTWQSURSQIA 207

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A.Geneseq_21:*

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1124	100.0	207	1 AAP60592	Aap60592 Sequence
2	1124	100.0	207	1 AAP6075	Aap6075 Sequence
3	1124	100.0	207	1 AAP60786	Aap60786 Sequence
4	1124	100.0	207	2 AA030309	Aaw30309 Human TIM
5	1124	100.0	207	2 AA089333	AAy08933 Human TIM
6	1124	100.0	207	3 AAB19073	Aab19073 Inhibitor
7	1124	100.0	207	7 ADC37139	Adc37139 Human tis
8	1124	100.0	207	7 ADU78829	Adt78829 Human tis
9	1124	100.0	207	8 ADG25251	Adg25251 Human TIM
10	1124	100.0	207	8 ADQ07367	Adq07367 Human tis
11	1124	100.0	207	8 ADP75947	Adp75947 Human TIM
12	1124	100.0	207	8 ADQ29674	Adq29674 Human COL
13	1124	100.0	207	8 ADP23249	Adp23249 PRO polyp
14	1124	100.0	207	8 ADU06696	Adu06696 Novel bro
15	1124	100.0	207	9 ADV70205	Adv70205 Tumor-ass
16	1124	100.0	207	9 ADY14618	Ady14618 PRO polyp
17	1124	100.0	207	9 AEB87782	Aeb87782 Human TIM
18	1121	99.7	207	1 AAP60593	Aap60593 Sequence
19	1120	99.6	207	4 AAG89171	Aag89171 Human sec
20	1119	99.6	207	4 AAG93377	Aag93377 Human pol
21	1119	99.6	207	8 ADL30920	Adl30920 Human pro
22	1118	99.5	207	8 ADZ70216	Adz70216 Human tis
23	1104	98.2	207	2 AAR65005	Aar65005 Human tis
24	1073.5	95.5	203	8 ADO28641	Ado28641 Human TIM

25	1034	92.0	204	5 ABP42206	Abp42206 Human ova
26	1010	89.9	580	5 AAU99889	Aau99889 rTAP1 fus
27	1009	89.8	184	5 AAU99875	Aau99875 Human tis
28	1009	89.8	184	8 ADG14621	Adg14621 Human TIM
29	1009	89.8	580	5 AAU99882	Aau99882 TAP1 fus1
30	995	88.5	207	2 AAR65003	Aar65003 Cattle ti
31	951	84.6	207	2 AAR65004	Aar65004 Pig tisau
32	895	79.6	166	8 ADR87602	Adr87602 Human TIM
33	892.5	79.4	206	2 AAR65006	Aar65006 Rabbit ti
34	827.5	73.6	205	2 AAR65007	Aar65007 Mouse tis
35	818	72.8	217	7 ADU45970	Adu45970 Rat Prote
36	782.5	69.6	183	3 AAB44149	Aab44149 Human can
37	779.5	69.4	207	2 AAR65008	Aar65008 Mouse tis
38	728.5	64.8	212	5 ABP42381	Abp42381 Human ova
39	715	63.6	162	5 ABP42434	Abp42434 Human ova
40	691	61.5	128	5 AAU99887	Aau99887 Human TIM
41	683	60.8	522	5 AAU99885	Aau99885 rN-TAP1 f
42	682	60.7	127	5 AAU99886	Aau99886 Human TIM
43	682	60.7	522	5 AAU99883	Aau99883 NTAP1 fus
44	587.5	52.3	136	8 ADO07052	Ado07052 Human pro
45	543	48.3	156	8 ADP45514	Adp45514 Human col

ALIGNMENTS

RESULT 1
AAP60592
ID AAP60592 standard; protein; 207 AA.

AC AAP60592;

DT 13-AUG-1991 (first entry)

DE Sequence of a human protein having erythroid potentiating activity (EPA).
Erythroid precursor growth; anaemia therapy.

OS Homo sapiens.

PN WO8602100-A.

PD 10-APR-1986.

PF 01-OCT-1984; 84US-00656590.

PR 01-OCT-1984; 84US-00656590.

PA (SANO) SANDOZ LTD.
(RESC) RECENTS OF UNIV OF CALIFO.

PI Brown E, Clark S, Golde DW, Casson JC, Hewick R, Westbrook CA;

DR WPI; 1986-106663/16.

PS N-PSDB; AAN60494.

PT Vectors contg. gene for protein having erythroid potentiating activity -
used for producing protein to stimulate growth and formation of erythroid
cells.

PS Disclosure: Fig 4; 59pp; English.

CC The inventors claim human and gibbon EPA proteins (AAP60592, AAP60593)
and cDNA that encodes EPA (AAN60494, AAN60495). The EPA protein has a
biological activity of at least about 1,000,000 units per mg of protein
and has an apparent molecular weight of about 28,000 daltons

XX Sequence 207 AA;

Query Match 100.0%; Score 1124; DB 1; Length 207;
Best Local Similarity 100.0%; Pred. No. 4.1e-109;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MAPFEPLASGILLMLLMIAPSRACCTVPPHPOTAFGNSDLVIRAKFVGTPEVNOGTLTYOR 60
Db 1 MAPFEPLASGILLMLLMIAPSRACCTVPPHPOTAFGNSDLVIRAKFVGTPEVNOGTLTYOR 60
QY 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNRSEEFLLAGKLQDGLLHIT 120
Db 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNRSEEFLLAGKLQDGLLHIT 120
QY 121 TCSFVAPMNSLSLAQRGFTKTYTGCECTVFPCLISPCKLQSGTHCLMTDQLQGSSEK 180
Db 121 TCSFVAPMNSLSLAQRGFTKTYTGCECTVFPCLISPCKLQSGTHCLMTDQLQGSSEK 180
QY 181 GFQSRHLACLPRPGLCTWQSLRSQIA 207
Db 181 GFQSRHLACLPRPGLCTWQSLRSQIA 207

RESULT 2
AAP60275
ID AAP60275 standard; protein; 207 AA.
XX
AC AAP60275;
XX
DT 25-MAR-2003 (revised)
DT 03-OCT-2002 (revised)
DT 08-AUG-1991 (first entry)
XX
DE Sequence of human natural inhibitor of collagenases (NIC).
XX
KM Metallo-proteinase inhibitor; wound healing; emphysema;
XX rheumatoid arthritis therapy; ulceration; tumour metastasis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..23
FT /label= signal
FT Protein 24..207
FT /note= "claimed"
FT Modified-site 53..55
FT /note= "potential glycosylation site"
FT Modified-site 101..103
FT /note= "potential glycosylation site"
XX
PN EP189784-A.
XX
PD 06-AUG-1986.
XX
PF 16-JAN-1986; 86EP-00100482.
XX
PR 18-JAN-1985; 85US-00692808.
XX
PA (SEAR ) SEARLE & CO G D.
XX
PI Galloway WA, Clisbold PM, McCullagh KG;
XX
DR MPI; 1986-205910/32.
XX
DR N-PSDB; AAN60277.
XX
PT New human natural inhibitor of collagenase - for treating e.g. rheumatoid
PT arthritis or ulceration, and new DNA sequences coding for it.
XX
PS Disclosure; Fig 2; 51pp; English.
XX
CC The patentors claim the AA SQ of human NIC, DNA sequences coding for NIC,
CC and its RNA analogues and plasmids contg. this DNA. NIC inhibits the
CC activity of metallo-proteinases, esp. of collagenase, proteoglycanase,
CC gelatinase or a leucocyte, macrophage or tumour cell metallo-proteinase.
CC (Updated on 03-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003
CC to correct PA field.)
XX
SQ Sequence 207 AA;

```

```

Query Match 100.0%; Score 1124; DB 1; Length 207;
Best Local Similarity 100.0%; Pred. No. 4,1e-109;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPFEPLASGILLMLLMIAPSRACCTVPPHPOTAFGNSDLVIRAKFVGTPEVNOGTLTYOR 60
Db 1 MAPFEPLASGILLMLLMIAPSRACCTVPPHPOTAFGNSDLVIRAKFVGTPEVNOGTLTYOR 60
QY 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNRSEEFLLAGKLQDGLLHIT 120
Db 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNRSEEFLLAGKLQDGLLHIT 120
QY 121 TCSFVAPMNSLSLAQRGFTKTYTGCECTVFPCLISPCKLQSGTHCLMTDQLQGSSEK 180
Db 121 TCSFVAPMNSLSLAQRGFTKTYTGCECTVFPCLISPCKLQSGTHCLMTDQLQGSSEK 180
QY 181 GFQSRHLACLPRPGLCTWQSLRSQIA 207
Db 181 GFQSRHLACLPRPGLCTWQSLRSQIA 207

RESULT 3
AAP60786
ID AAP60786 standard; protein; 207 AA.
XX
AC AAP60786;
XX
DT 25-MAR-2003 (revised)
DT 08-AUG-1991 (first entry)
XX
DE Sequence of tissue inhibitor of metalloproteinase (TIMP).
XX
KM Connective tissue; extracellular matrix.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..23
FT /label= signal
FT Protein 24..207
FT Modified-site 53..55
FT /label= potential N-glycosylation site
FT Modified-site 101..103
FT /label= as above
XX
PN GB2169295-A.
XX
PD 09-JUL-1986.
XX
PF 06-JAN-1986; 86GB-00000199.
XX
PR 05-OCT-1983; 83BE-00897924.
PR 07-JAN-1985; 85GB-00000341.
PR 07-JAN-1985; 85GB-00500341.
PR 01-NOV-1985; 85GB-00026951.
XX
PA (CLLT ) CELLTech LTD.
XX
PI Harris TUR, Reynolds JJ, Docherty ALP, Murphy G;
XX
DR MPI; 1986-177873/28.
XX
DR N-PSDB; AAN60538.
XX
PT Prodn. of metallo-proteinase inhibitors - by recombinant DNA techniques.
XX
PS Disclosure; Fig 3; 16pp; English.
XX
CC A gene with residues 64-684 of AAN60538 is claimed. AAN60538 was isolated
CC from human a foetal diploid lung cells (ATCC CCL153) cDNA library using
CC AAN60539. (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 207 AA;

```

Query Match 100.0%; Score 1124; DB 1; Length 207;
 Best Local Similarity 100.0%; Pred. No. 4.1e-109;
 Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPEPLASGILLMLIAPSRACVCPHPQTAFCNSDLVIRAKFVGTPEVNOGTLTYOR 60
 DB 1 MAPEPLASGILLMLIAPSRACVCPHPQTAFCNSDLVIRAKFVGTPEVNOGTLTYOR 60
 QY 61 YEIKTKMYKGFQALGDAADIRFYVTPAMESVCYGFHSHNRSEEFLLAGKLDGGLHIT 120
 DB 61 YEIKTKMYKGFQALGDAADIRFYVTPAMESVCYGFHSHNRSEEFLLAGKLDGGLHIT 120
 QY 121 TCSFVAPWNSLSLAQRGFTKTYTVGCECTVPCLSI PCKLQSGTHCLMTDQLQSGSEK 180
 DB 121 TCSFVAPWNSLSLAQRGFTKTYTVGCECTVPCLSI PCKLQSGTHCLMTDQLQSGSEK 180
 QY 181 GFQSRHLACLPRPGLCTWQSLRSQIA 207
 DB 181 GFQSRHLACLPRPGLCTWQSLRSQIA 207

RESULT 4
 AAW30309
 ID AAW30309 standard; protein; 207 AA.
 AC AAW30309;
 XX
 DT 29-JAN-1998 (first entry)
 DE Human TIMP-1.
 XX
 KW TIMP-3; human; antibody; TIMP-3-mediated disease; malignant tumour cell;
 KW cancer progression; TIMP-1.
 XX
 OS Homo sapiens.
 XX
 PN JP09235300-A.
 XX
 PD 09-SEP-1997.
 XX
 PF 29-FEB-1996; 96JP-00067484.
 XX
 PR 29-FEB-1996; 96JP-00067484.
 XX
 PA (FUJY) FUJY PHARM IND CO LTD.
 XX
 DR WPI; 1997-498341/46.
 DR N-PSDB; AAT92631.
 XX
 PT Human TIMP-3 and anti-human TIMP-3 monoclonal antibodies - used in
 PT diagnosis of TIMP-3 mediated disease, especially the detection of
 PT malignant tumour cells.
 XX
 PS Example 12; Page 33-34; 37pp; Japanese.
 XX
 CC This sequence represents the human TIMP-1 protein. This sequence was used
 CC to test the specificity of the monoclonal antibody (MAb) of the
 CC invention. The MAb of the invention reacts specifically with human TIMP-3
 CC (see AAW30309), by specific recognition of the TIMP-3 fragments
 CC represented by AAW30305-W30307. The MAb can be used in the study or
 CC diagnosis of TIMP-3-mediated diseases, particularly for the detection of
 CC malignant tumour cells, or the diagnosis of progressiveness of cancers.
 CC They can also be used in establishing an immunoassay for TIMP-3 or in
 CC purification of TIMP-3. The transformed cells can be used for producing
 CC TIMP-3 or its equivalent proteins on a large scale. The immunoassay
 CC method for TIMP-3 the MAbs is simple, highly reproducible and highly
 CC sensitive
 CC
 SQ Sequence 207 AA;
 Query Match 100.0%; Score 1124; DB 2; Length 207;
 Best Local Similarity 100.0%; Pred. No. 4.1e-109;
 Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPEPLASGILLMLIAPSRACVCPHPQTAFCNSDLVIRAKFVGTPEVNOGTLTYOR 60
 DB 1 MAPEPLASGILLMLIAPSRACVCPHPQTAFCNSDLVIRAKFVGTPEVNOGTLTYOR 60
 QY 61 YEIKTKMYKGFQALGDAADIRFYVTPAMESVCYGFHSHNRSEEFLLAGKLDGGLHIT 120
 DB 61 YEIKTKMYKGFQALGDAADIRFYVTPAMESVCYGFHSHNRSEEFLLAGKLDGGLHIT 120
 QY 121 TCSFVAPWNSLSLAQRGFTKTYTVGCECTVPCLSI PCKLQSGTHCLMTDQLQSGSEK 180
 DB 121 TCSFVAPWNSLSLAQRGFTKTYTVGCECTVPCLSI PCKLQSGTHCLMTDQLQSGSEK 180
 QY 181 GFQSRHLACLPRPGLCTWQSLRSQIA 207
 DB 181 GFQSRHLACLPRPGLCTWQSLRSQIA 207

RESULT 5
 AAY08933
 ID AAY08933 standard; protein; 207 AA.
 AC AAY08933;
 XX
 DT 19-AUG-1999 (first entry)
 DE Human TIMP-1 protein.
 XX
 KW TIMP-4; tissue inhibitor of metalloprotease; human; antibody; diagnosis;
 KW treatment; metastasis; neoplastic cell; angiogenesis; tumour; cervical;
 KW uterine; pancreatic; colon; intestinal carcinoma; pregnancy; ulcer;
 KW osteoarthritis; pulmonary emphysema; periodontal disease; corneal;
 KW rheumatoid arthritis; diabetic ulcer; lesion; TIMP-4.
 XX
 OS Homo sapiens.
 XX
 PN US5914392-A.
 XX
 PD 22-JUN-1999.
 XX
 PF 07-JUL-1998; 98US-00111070.
 XX
 PR 18-JAN-1996; 96US-00588163.
 PR 27-JUN-1997; 97US-00884073.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Murry LE, Hawkins PR;
 XX
 DR WPI; 1999-384187/32.
 XX
 PT Anti-tissue inhibitor metalloproteinase antibodies useful for treating
 PT and diagnosing cancer.
 XX
 PS Disclosure; Fig 4; 26pp; English.
 XX
 CC This invention describes a novel method for the production of antibodies
 CC specific for the human tissue inhibitors of metalloproteinase 4, TIMP-4.
 CC The anti-TIMP-4 antibodies may be used to treat, prevent or diagnose
 CC metastasis of neoplastic cells, angiogenesis and growth tumours such as
 CC cervical, uterine, pancreatic, colon or intestinal carcinomas, pregnancy,
 CC osteoarthritis, pulmonary emphysema, periodontal disease, rheumatoid
 CC arthritis, corneal or diabetic ulcers or ulcers and lesions caused by
 CC microorganisms. This sequence represents TIMP-4 which is used to describe
 CC the method of the invention
 CC
 SQ Sequence 207 AA;
 Query Match 100.0%; Score 1124; DB 2; Length 207;
 Best Local Similarity 100.0%; Pred. No. 4.1e-109;
 Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Db      1 MAFPEPLASGILLMLLAPSRACVCPHPQTAFCNSDLVIRAKFVGPEVNQTTLYOR 60
Qy      61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSEEFLLAGKLODGLLHTT 120
Db      61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSEEFLLAGKLODGLLHTT 120
Qy      121 TCSFVAPMNSLSLAORRGFTKTYTGCECTVPCLSIPCKLOSGTHCLMTDQLQGSSEK 180
Db      121 TCSFVAPMNSLSLAORRGFTKTYTGCECTVPCLSIPCKLOSGTHCLMTDQLQGSSEK 180
Qy      181 GFQSRHLACLPREPGICTWQSLRSQIA 207
Db      181 GFQSRHLACLPREPGICTWQSLRSQIA 207

RESULT 6
AAB19073
ID      AAB19073 standard; protein; 207 AA.
XX
AC      AAB19073;
XX
DT      08-FEB-2001 (first entry)
XX
DE      Inhibitor of tissue metalloproteinase designated TIMP-1.
XX
KM      Tissue metalloproteinase inhibitor; TIMP; metalloproteinase; gelatinase;
XX      metastasis; cancer.
XX
OS      Unidentified.
XX
FH      Key
FT      Peptide      Location/Qualifiers
FT      Protein      1..23
FT      Protein      /note="signal peptide"
FT      Protein      24..207
FT      Protein      /note="mature protein"

EP1041083-A1.
XX
PN      04-OCT-2000.
XX
PF      03-APR-2000; 2000BP-00107041.
XX
PR      01-APR-1999; 99JP-00095142.
XX
PA      (ORLY ) ORIENTAL YEAST CO LTD.
XX
PI      Miyazaki K, Higashi S;
XX
DR      WPI; 2000-603818/58.
XX
PT      New modified tissue inhibitor of metalloproteinases, useful for
XX      manufacturing compositions for inhibiting metastasis of cancer and
XX      vascularization and for preventing or treating diseases associated with
XX      these, e.g. brain tumor.
XX
PS      Disclosure; Page 12-13; 25pp; English.
XX
CC      The present sequence represents an inhibitor of tissue metalloproteinase,
XX      designated TIMP. The specification describes modified forms of TIMP,
XX      where the amino-terminal alpha-amino group is modified with an electron
XX      accepting group to substantially lose the ability to bind to a
XX      metalloproteinase. Modified TIMP-2 prevents an accumulation of active
XX      gelatinase. A on the cell surface, and can inhibit the activation of
XX      precursor matrix metalloproteinases. The modified TIMP-2 and the
XX      compositions comprising TIMP-2 are useful for inhibiting metastasis of
XX      cancer and vascularisation. It is also used for treating diseases
XX      associated with them. Specifically, these are useful for preventing or
XX      treating metastasis of cancer of the stomach, colon, lung, head and neck,
XX      brain tumour, breast, thyroid, prostate, ovary or pancreas, or
XX      vascularisation or other conditions associated with these
XX      Sequence 207 AA;
XX
```

```
Query Match      100.0%; Score 1124; DB 3; Length 207;
Best Local Similarity 100.0%; Pred. No. 4.1e-109;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MAFPEPLASGILLMLLAPSRACVCPHPQTAFCNSDLVIRAKFVGPEVNQTTLYOR 60
Db      1 MAFPEPLASGILLMLLAPSRACVCPHPQTAFCNSDLVIRAKFVGPEVNQTTLYOR 60
Qy      61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSEEFLLAGKLODGLLHTT 120
Db      61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSEEFLLAGKLODGLLHTT 120
Qy      121 TCSFVAPMNSLSLAORRGFTKTYTGCECTVPCLSIPCKLOSGTHCLMTDQLQGSSEK 180
Db      121 TCSFVAPMNSLSLAORRGFTKTYTGCECTVPCLSIPCKLOSGTHCLMTDQLQGSSEK 180
Qy      181 GFQSRHLACLPREPGICTWQSLRSQIA 207
Db      181 GFQSRHLACLPREPGICTWQSLRSQIA 207

RESULT 7
ADC37139
ID      ADC37139 standard; protein; 207 AA.
XX
AC      ADC37139;
XX
DT      18-DEC-2003 (first entry)
XX
DE      Human tissue inhibitor of metalloproteinase-1 (TIMP-1) protein.
XX
KM      liver fibrosis; alpha-2-macroglobulin; alpha-2-MG; hyaluronic acid; HA;
XX      tissue inhibitor of metalloproteinases-1; TIMP-1; anti-fibrotic therapy;
XX      human.
XX
OS      Homo sapiens.
XX
PN      WO2003073822-A2.
XX
PD      12-SEP-2003.
XX
PF      28-FEB-2003; 2003WO-US006038.
XX
PR      28-FEB-2002; 2002US-00087188.
XX
PA      (PROM-) PROMETHEUS LAB INC.
XX
PI      Rose SL, Oh EH, Walsh MJ;
XX
DR      WPI; 2003-756744/71.
XX
DR      N-PDB; ADC37138.
XX
PT      Diagnosing the presence or severity of liver fibrosis in an individual by
XX      detecting alpha2-macroglobulin, hyaluronic acid or detecting tissue
XX      inhibitor of metalloproteinases-1 in a sample from the individual.
XX
PS      Disclosure; SEQ ID NO 4; 133pp; English.
XX
CC      The invention relates to a novel method for diagnosing the presence or
XX      severity of liver fibrosis in an individual. The novel method comprises:
XX      detecting alpha-2-macroglobulin (alpha-2-MG) in a sample from the
XX      individual; detecting hyaluronic acid (HA) in a sample from the
XX      individual; detecting tissue inhibitor of metalloproteinases-1 (TIMP-1)
XX      in a sample from the individual; and diagnosing the presence or severity
XX      of liver fibrosis in the individual based on the presence or level of
XX      alpha-2-MG, HA and TIMP-1. The methods are useful for diagnosing the
XX      presence or severity of liver fibrosis in an individual, differentiating
XX      no or mild liver fibrosis in an individual to severe liver fibrosis, and
XX      monitoring the efficacy of anti-fibrotic therapy in a patient. This
XX      sequence represents the human tissue inhibitor of metalloproteinase-1
XX      (TIMP-1) protein of the invention.
XX
```


SQ Sequence 207 AA;

Query Match 100.0%; Score 1124; DB 7; Length 207;
 Best Local Similarity 100.0%; Pred. No. 4,1e-109; Indels 0; Gaps 0;
 Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPEPLASGILLMLLAPSRACVPPHPQTAFCNSDLVIRAKFVGPVNOQTLYOR 60
 Db 1 MAPEPLASGILLMLLAPSRACVPPHPQTAFCNSDLVIRAKFVGPVNOQTLYOR 60
 QY 61 YEIKMTKMYKGFQALGDADIRFVYTPPAMESVCGYFHRSHNRSEBFLIAGKLODGLIHT 120
 Db 61 YEIKMTKMYKGFQALGDADIRFVYTPPAMESVCGYFHRSHNRSEBFLIAGKLODGLIHT 120
 QY 121 TCSFVAPWNSLSAQRGFTKTYTGCECTVPCLSTPCKLQSGTHCLMTDOLLOQSEK 180
 Db 121 TCSFVAPWNSLSAQRGFTKTYTGCECTVPCLSTPCKLQSGTHCLMTDOLLOQSEK 180
 QY 181 GFQSRHLACLPRPGLCTWQSLRSQIA 207
 Db 181 GFQSRHLACLPRPGLCTWQSLRSQIA 207

RESULT 8
 ADL78829
 ID ADL78829 standard; protein; 207 AA.

AC ADL78829;
 DT 20-MAY-2004 (first entry)

DE Human tissue inhibitor of metalloproteinase-1 (TIMP-1).

XX
 KW vasoactive; antistatic; dermatological; nephrotoxic; antineumatic;
 KW antiarthritic; antiprotatic; osteopathic; cytosolic; vulnerary;
 KW antitumor; antitumor; neuroprotective; antibacterial;
 KW immunosuppressive; metalloproteinase inhibitor;
 KW tissue inhibitor of metalloproteinase 4; TIMP-4; restenosis; arthritis;
 KW soft tissue rheumatism; polychondritis; tendonitis;
 KW bone resorption disease; osteoporosis; Paget's disease; hyperthyroidism;
 KW cholesteatoma; collagen destruction; diabetes;
 KW dystrophic epidermolysis bullosa; periodontal disease; alveolitis;
 KW gingival production of collagenase; corneal ulceration; skin ulceration;
 KW gastro-intestinal tract ulceration; wound healing; cancer;
 KW demyelinating disease; asthma; glomerulosclerosis; septic shock;
 KW infection; psoriasis; human; TIMP-1;
 KW tissue inhibitor of metalloproteinase 1.

XX Homo sapiens.

OS US2003157687-A1.

PN 21-AUG-2003.

XX 14-FEB-2003; 2003US-00366445.

XX 13-DEC-1994; 94WO-US014498.

XX 05-JUN-1995; 95US-00463261.

XX 01-SEP-1999; 99US-00387525.

XX 11-JUL-2000; 2000US-0217419P.

XX 26-JUL-2000; 2000US-0220839P.

XX 11-JUL-2001; 2001US-00901904.

XX (GREGG) GREENE J M.

XX (ROSE) ROSEN C A.

XX Greene JM, Rosen CA;
 PI WPI; 2003-897817/82.

PT New polynucleotide encoding a tissue inhibitor of metalloproteinase
 PT designated TIMP-4 is useful to treat metalloproteinase associated disease
 PT including restenosis and collagenase-associated disease.

XX Disclosure; Fig 2; 61pp; English.

XX The invention describes an isolated polynucleotide encoding a tissue
 CC inhibitor of metalloproteinase designated TIMP-4. The invention is used
 CC to treat restenosis. Other disease which may be treated include arthritic
 CC diseases such as rheumatoid and osteoarthritis, soft tissue rheumatism,
 CC polychondritis and tendonitis, bone resorption diseases such as
 CC osteoporosis, Paget's disease, hyperthyroidism and cholesteatoma, the
 CC enhanced collagen destruction that occurs with diabetes, the recessive
 CC classes of dystrophic epidermolysis bullosa, periodontal disease,
 CC alveolitis and related consequences of gingival production of
 CC collagenase, corneal ulceration, ulceration of the skin and gastro-
 CC intestinal tract and abnormal wound healing, post-operative conditions in
 CC which collagenase levels are raised, cancer by blocking the destruction
 CC of tissue basement membranes leading to cancer metastases, demyelinating
 CC disease of the central and peripheral nervous systems, asthma,
 CC glomerulosclerosis, septic shock and infection, and psoriasis. This is
 CC the amino acid sequence of human tissue inhibitor of metalloproteinase-1
 CC (TIMP-1) used in a comparison with TIMP-4 of the invention.

XX SQ Sequence 207 AA;

Query Match 100.0%; Score 1124; DB 7; Length 207;
 Best Local Similarity 100.0%; Pred. No. 4,1e-109; Indels 0; Gaps 0;
 Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPEPLASGILLMLLAPSRACVPPHPQTAFCNSDLVIRAKFVGPVNOQTLYOR 60
 Db 1 MAPEPLASGILLMLLAPSRACVPPHPQTAFCNSDLVIRAKFVGPVNOQTLYOR 60
 QY 61 YEIKMTKMYKGFQALGDADIRFVYTPPAMESVCGYFHRSHNRSEBFLIAGKLODGLIHT 120
 Db 61 YEIKMTKMYKGFQALGDADIRFVYTPPAMESVCGYFHRSHNRSEBFLIAGKLODGLIHT 120
 QY 121 TCSFVAPWNSLSAQRGFTKTYTGCECTVPCLSTPCKLQSGTHCLMTDOLLOQSEK 180
 Db 121 TCSFVAPWNSLSAQRGFTKTYTGCECTVPCLSTPCKLQSGTHCLMTDOLLOQSEK 180
 QY 181 GFQSRHLACLPRPGLCTWQSLRSQIA 207
 Db 181 GFQSRHLACLPRPGLCTWQSLRSQIA 207

RESULT 9
 ADG25251
 ID ADG25251 standard; protein; 207 AA.

XX ADG25251;

XX 26-FEB-2004 (first entry)

DE Human TIMP-1 #SEQ ID 20.

XX Antinflammatory; hypotensive; antiallergic; immunosuppressive;
 KW antistatic; protease; lipase; inhibitor; lung surfactant;
 KW pulmonary inflammation; emphysema; pneumonia; human.

XX Homo sapiens.

OS WO2003090682-A2.

XX 06-NOV-2003.

XX 25-APR-2003; 2003WO-US012731.

XX 25-APR-2002; 2002US-0375968P.

XX (SCRI) SCRIPPS RES INST.

XX Cochran CG, Oades ZG, Revak SD, Niven R;
 PI WPI; 2004-132634/13.

XX Composition useful for treating pulmonary inflammation e.g. chronic
PT obstructive pulmonary disease comprises a lung surfactant polypeptide and
PT a protease inhibitor.
XX
XX
PS Claim 6; SEQ ID NO 20; 137pp; English.
XX
XX The invention relates to a liquid aerosolised composition, comprising a
CC lung surfactant polypeptide and a protease inhibitor. The composition is
CC useful for treating pulmonary inflammation (e.g. inflammation associated
CC with pulmonary hypertension, neonatal pulmonary hypertension, neonatal
CC bronchopulmonary dysplasia, chronic obstructive pulmonary disease, acute
CC or chronic bronchitis, emphysema, bronchiolitis, bronchiectasis,
CC radiation pneumonitis, hypersensitivity, pneumonitis, acute inflammatory
CC asthma, acute smoke inhalation, thermal lung injury, allergic asthma,
CC iatrogenic aschma, cystic fibrosis, alveolar proteinosis, alpha-1-
CC protease deficiency, pulmonary inflammatory disorders, pneumonia, acute
CC respiratory distress syndrome, acute lung injury, idiopathic respiratory
CC distress syndrome, and idiopathic pulmonary fibrosis). The current
CC sequence represents a protease inhibitor that may be part of a
CC composition of the invention.
XX
SQ Sequence 207 AA;
Query Match 100.0%; Score 1124; DB 8; Length 207;
Best Local Similarity 100.0%; Pred. No. 4.1e-109;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPPEPLASGILLLMLLIPSRACCTVPPHPOTAFNSDLVIRAKVGPEVNQTLVQR 60
DB 1 MAPPEPLASGILLLMLLIPSRACCTVPPHPOTAFNSDLVIRAKVGPEVNQTLVQR 60
QY 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSSEFLIAGKLQDGLHIT 120
DB 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSSEFLIAGKLQDGLHIT 120
QY 121 TCSFVAPMNSLSLAORRGFTKTYTVGCEBCTVFPCLISIPCKLQSGTHCLMTDQLQGSBK 180
DB 121 TCSFVAPMNSLSLAORRGFTKTYTVGCEBCTVFPCLISIPCKLQSGTHCLMTDQLQGSBK 180
QY 181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
DB 181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
RESULT 10
ADQ07367
ID ADQ07367 standard; protein; 207 AA.
XX
XX ADQ07367;
AC
XX
DT 09-SEP-2004 (first entry)
XX
DE Human tissue inhibitor of metalloproteinase 1 (TIMP1).
XX
XX matrix metalloproteinase; MMP; MMP inhibitor; proteinase inhibitor;
KW scar prevention; skin development; human;
KW tissue inhibitor of metalloproteinase 1; TIMP-1; wound healing; skin;
KM enzyme.
XX
XX Homo sapiens.
OS
XX
PN US2004121438-A1.
XX
PD 24-JUN-2004.
XX
XX 19-DEC-2002; 2002US-00325446.
XX
PF 19-DEC-2002; 2002US-00325446.
XX
PR 19-DEC-2002; 2002US-00325446.
XX
XX (QIIR/) QIIRK S.
PA
XX
PI Quick S;

XX
DR WPI; 2004-479683/45.
XX
XX
PT New wound care compositions, useful in promoting wound healing,
PT preventing scarring, improving skin tone, and in stimulating the
PT development of a smooth, healthy skin.
XX
XX
PS Disclosure; SEQ ID NO 1; 43pp; English.
XX
XX The invention describes an isolated nucleic acid (I). (I) comprises a
CC sequence: encoding a polypeptide comprising a sequence of 108 amino acids
CC (SEQ ID NOS: 5 or 20); or which hybridises under stringent hybridisation
CC conditions to a nucleic acid comprising a sequence of 339 bp (SEQ ID NO:
CC 6). Also described are: an isolated polypeptide comprising SEQ ID NOS: 5
CC or 20 or comprising SEQ ID NOS: 7 or 21 that has a beta barrel
CC conformation and that can bind to a matrix metalloproteinase; a
CC composition comprising a therapeutic amount of polypeptide or
CC polypeptide inhibitor comprising SEQ ID NOS: 5, 7, 20 or 21 and a
CC pharmaceutical carrier, where the polypeptide or polypeptide inhibitor
CC can inhibit proteinase activity of matrix metalloproteinase-1 to -13; a
CC wound dressing comprising a polypeptide of (I) and a pharmaceutical
CC carrier; and treating a wound comprising administering a therapeutical
CC amount of a polypeptide of (I) to the wound. (I) is nucleic acid
CC comprising a sequence of 339 bp (SEQ ID NO: 6) encoding wound care
CC compositions comprising a sequence of 108 amino acids (SEQ ID NOS: 5 or
CC 20). The nucleic acid and the encoded polypeptide, composition, and
CC method are useful in promoting wound healing, preventing scarring,
CC improving skin tone, and in stimulating the development of a smooth,
CC healthy skin. This is the amino acid sequence of human tissue inhibitor
CC of metalloproteinase 1 (TIMP-1), useful in wound healing and promoting
XX development of healthy skin.
SQ Sequence 207 AA;
Query Match 100.0%; Score 1124; DB 8; Length 207;
Best Local Similarity 100.0%; Pred. No. 4.1e-109;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPPEPLASGILLLMLLIPSRACCTVPPHPOTAFNSDLVIRAKVGPEVNQTLVQR 60
DB 1 MAPPEPLASGILLLMLLIPSRACCTVPPHPOTAFNSDLVIRAKVGPEVNQTLVQR 60
QY 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSSEFLIAGKLQDGLHIT 120
DB 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSSEFLIAGKLQDGLHIT 120
QY 121 TCSFVAPMNSLSLAORRGFTKTYTVGCEBCTVFPCLISIPCKLQSGTHCLMTDQLQGSBK 180
DB 121 TCSFVAPMNSLSLAORRGFTKTYTVGCEBCTVFPCLISIPCKLQSGTHCLMTDQLQGSBK 180
QY 181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
DB 181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
RESULT 11
ADP75947
ID ADP75947 standard; protein; 207 AA.
XX
XX ADP75947;
AC
XX
DT 09-SEP-2004 (first entry)
XX
DE Human TIMP1 protein differentially expressed in schizophrenia; Seq 151.
XX
XX tissue inhibitor of metalloproteinase 1; human; schizophrenia; SCV2;
KW GAD5B; S100A8; CDKN1A; IL1RL1; TGM2; MAF; SERPIN3; GRI1; CD14;
KW KIAA1075; CH13L1; SERPINH1; MTIX; KIAA0620; TIMP1; NUMA1; DDT13; TOB2;
KW neuroleptic; gene therapy.
XX
XX Homo sapiens.
OS
XX
PN WO2004053157-A2.

XX 24-JUN-2004.
 PD
 XX 11-DEC-2003; 2003WO-EP014089.
 XX
 PF 12-DEC-2002; 2002US-0432853P.
 XX
 PR (NOVUS) NOVARTIS AG.
 XX (NOVUS) NOVARTIS PHARMA GMBH.
 PA (UTMA) UNITIV MARYLAND BALTIMORE.
 XX
 XX Buxton FP, Carpenter WT, Roberts RC, Tamminga CA;
 PI
 XX MPI; 2004-507015/48.
 DR N-PSDB; ADP755928.
 XX
 XX Screening or diagnosing schizophrenia comprises determining the magnitude
 PT of expression of at least one gene upregulated in the anterior cingulate.
 XX
 PS Example 2; SEQ ID NO 151; 63pp; English.
 XX
 CC Screening for schizophrenia in a population or diagnosing schizophrenia
 CC in a host comprises determining the magnitude of expression, in members
 CC of the population, of at least one of the 19 genes (SCYA2, GAD65B,
 CC S100A8, CDKN1A, IL1RL1, TGM2, MAFK, SERPINA3, GRI1, CD14, KIA1075,
 CC CH13L1, SERP1H1, MTX1, KIA0620, TIMP1, NDUAF1, DDIR3, or TOS2) in a
 CC sample. Screening for schizophrenia in a population or diagnosing
 CC schizophrenia in a host comprises: determining the magnitude of
 CC expression, in members of the population, of at least one of the 19 genes
 CC in a sample; and comparing the magnitude of expression to a baseline
 CC magnitude of expression of the gene, where increased gene expression
 CC indicates the presence of schizophrenia. INDEPENDENT CLAIMS are also
 CC included for: treating schizophrenia in a host; a transgenic nonhuman
 CC animal comprising stably integrated in its genome an increased copy
 CC number of any of the 19 genes, where expression of the gene is enhanced
 CC by one or more alterations in regulatory sequences of the gene such that
 CC the gene is expressed at higher than baseline levels and the animal
 CC exhibits schizophrenic behavior or a transgenic nonhuman knockout animal
 CC whose genome comprises a homozygous disruption in one or more of the 19
 CC genes, where the homozygous disruption prevents the expression of the
 CC gene, and where the homozygous disruption results in the transgenic
 CC knockout animal exhibiting decreased expression levels of the one or more
 CC genes as compared to a wild-type animal; screening for a therapeutic
 CC agent that modulates symptoms of schizophrenia; and screening for a
 CC compound useful in treating schizophrenia. Preferred Method: The sample
 CC is taken from brain, spinal cord, lymphatic fluid, blood, urine or feces.
 CC The sample is taken from the anterior cingulate. The population or host
 CC is human. Treating schizophrenia in a host comprises lowering expression
 CC of at least one of the 19 genes by administering to the host an
 CC expression lowering amount of antisense oligonucleotide; an expression
 CC lowering amount of a ribozyme which cleaves RNA associated with
 CC expression of the gene; one or more nucleic acid molecules designed to
 CC promote triple helix formation with the gene; or one or more RNAi
 CC molecules designed to inhibit the expression of the gene. Alternatively,
 CC the method comprises reducing the amount of at least one protein encoded
 CC by any of the 19 genes in a patient by administering an amount of
 CC antibody or functional antibody fragment to interfere with the normal
 CC activity of the protein. The antibody or functional antibody fragment is
 CC whole antibody, humanized antibody, chimeric antibody, Fab fragment, Fab'
 CC fragment, F(ab')₂ fragment, single chain Fv fragment, or diabody.
 CC Screening for a therapeutic agent that modulates symptoms of
 CC schizophrenia comprises administering a candidate compound to a
 CC transgenic nonhuman animal of (2) or combining a candidate compound with
 CC a transgenic nonhuman animal of (2) and determining the effect of the
 CC compound on symptoms associated with schizophrenia. Screening for a
 CC compound, useful in treating schizophrenia, comprises operatively linking
 CC a reporter gene which expresses a detectable protein to a regulatory
 CC sequence for any of the 19 genes to produce a reporter construct,
 CC transfecting a cell with the reporter construct, exposing the transfected
 CC cell to a test compound and comparing the level of expression of the
 CC reporter gene before and after exposure to the test compound, where a
 CC lower level of expression after exposure is indicative of a compound
 CC useful for the treatment of schizophrenia. Preferred Transgenic Nonhuman

CC Animal: The transgenic nonhuman animal is a mammal. One or more
 CC alterations comprise substitution of a promoter having a higher rate of
 CC expression than the native promoter of the gene. The promoter is an
 CC inducible promoter. Neuroleptic. No biological data given. Gene therapy.
 CC Dosage is 0.1-100000 μ g/kg, by topical, pulmonary, intratracheal,
 CC intranasal, enteral, epidermal and transdermal, oral, sublingual, buccal
 CC or parenteral including intravenous, intraarterial, subcutaneous,
 CC intraperitoneal, intramuscular, infusion, intramedullary, intracranial,
 CC intrathecal or intraventricular means. The method is useful for screening
 CC for schizophrenia in a population or diagnosing schizophrenia in a host.
 CC The methods, compounds and compositions are useful in treating
 CC schizophrenia.
 CC
 XX
 SQ Sequence 207 AA;
 Query Match 100.0%; Score 1124; DB 8; Length 207;
 Best Local Similarity 100.0%; Pred. No. 4.1e-109;
 Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAFEPPLASGILLMLTAPSRACVPHPTARCNSTLVIRAKVGTPEVNGTTLXOR 60
 DB 1 MAFEPPLASGILLMLTAPSRACVPHPTARCNSTLVIRAKVGTPEVNGTTLXOR 60
 QY 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHSRSHNSSEFLIAGKIQDGLHIT 120
 DB 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHSRSHNSSEFLIAGKIQDGLHIT 120
 QY 121 TCSFVAPMNSLSLAQRGFTKYTVGCECTVFPCLSIPTCKIQSGTHCLMTDQLQGSER 180
 DB 121 TCSFVAPMNSLSLAQRGFTKYTVGCECTVFPCLSIPTCKIQSGTHCLMTDQLQGSER 180
 QY 181 GFQSRHIACTPREBGLCTWQSLRSQIA 207
 DB 181 GFQSRHIACTPREBGLCTWQSLRSQIA 207
 RESULT 12
 ADQ29674
 ID ADQ29674 standard; protein; 207 AA.
 XX
 AC ADQ29674;
 XX
 DT 07-OCT-2004 (first entry)
 XX
 DE Human colorectal cancer-associated protein #29.
 XX
 KW human; colon cancer; TIMP1; Reg1-alpha;
 XX colorectal cancer-associated marker.
 OS Homo sapiens.
 XX
 PN EP1439393-A2.
 XX
 PD 21-JUL-2004.
 XX
 PF 15-DEC-2003; 2003EP-00257868.
 XX
 PR 13-DEC-2002; 2002US-0433554P.
 XX
 PR 31-JUL-2003; 2003US-0491397P.
 XX
 PA (FARB) BAYER HEALTHCARE LLC.
 XX (MAYO) MAYO FOUND MEDICAL EDUCATION & RES.
 XX
 PI Astle JH, Boardman LA, Bugart LJ, Burgess CC, Catino TJ,
 XX Dwyerdi P, Huntress M, Johnson KA, Lewis ME, Maimonis PJ, Myerow SH;
 PI Brown-Shiner SLA, Thiagalingam A, Thibodeau SN, Molino GA;
 XX
 DR MPI; 2004-545561/53.
 N-PSDB; ADQ29607.
 PT
 PT Diagnosing colon cancer in individual, preferably human, by detecting
 PT presence of TIMP 1 in sample, where presence of TIMP 1 in sample is
 PT indicative of colon cancer in individual.

```
XX Claim 7; SEQ ID NO 100; 433bp; English.
PS
XX
CC The invention comprises a method for diagnosing colon cancer in an
CC individual, the method involves obtaining a serum sample from the
CC individual and detecting the presence of either TIMP1 or Reg1-alpha and
CC an additional colorectal cancer-associated marker. The method of the
CC invention is useful for diagnosing colon cancer in an individual. The
CC present amino acid sequence represents a human colorectal cancer-
CC associated protein of the invention.
XX
SQ
XX Sequence 207 AA;
Query Match 100.0%; Score 1124; DB 8; Length 207;
Best Local Similarity 100.0%; Pred. No. 4.1e-109;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPFEPLASGILLMLLIPSRACCTVPPHPQTAFNCNSDLVIRAKFVGTPENVQTTLYQR 60
DB 1 MAPFEPLASGILLMLLIPSRACCTVPPHPQTAFNCNSDLVIRAKFVGTPENVQTTLYQR 60
QY 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSSEFLIAGKLDGLLHIT 120
DB 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSSEFLIAGKLDGLLHIT 120
QY 121 TCSFVAPMNSLSIAORRGFTKTYTGCECTVFPCLSIIPCKLQSGTHCLMTDQLQGSSEK 180
DB 121 TCSFVAPMNSLSIAORRGFTKTYTGCECTVFPCLSIIPCKLQSGTHCLMTDQLQGSSEK 180
QY 181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
DB 181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
RESULT 13
ADP23249
ID ADP23249 standard; protein; 207 AA.
XX
AC ADP23249;
XX
DT 18-NOV-2004 (first entry)
XX
DE PRO polypeptide SEQ ID NO:343.
XX
KM PRO: antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
KM osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;
KM antiaesthetic; hepatotropic; respiratory; gene therapy; immune system.
XX
OS Unidentified.
XX
PN WO2004041170-A2.
XX
PD 21-MAY-2004.
XX
PF 30-OCT-2003; 2003WO-US034312.
XX
PR 01-NOV-2002; 2002US-0423394P.
XX
PA (GETH ) GENENTECH INC.
XX
PI Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
PI Wu TD;
XX
DR WPI; 2004-419628/39.
XX
DR N-PSDB; ADP23248.
XX
PT New PRO polypeptides and polynucleotides, useful for treating e.g.
PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
PT renal disease, or demyelinating diseases of the central or peripheral
PT nervous system.
XX
PS Claim 7; SEQ ID NO 343; 2940bp; English.
XX
```

```
CC The invention relates to a novel isolated nucleic acid and the PRO
CC polypeptide encoded by it. A protein of the invention has
CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
CC antiaesthetic, hepatotropic, and respiratory activity. A polynucleotide
CC of the invention may have a use in gene therapy. The PRO polypeptide, its
CC agonist, antagonist, or antibody that specifically binds to the
CC polypeptide is useful for treating an immune related disorder such as
CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
CC disease, a demyelinating disease of the central or peripheral nervous
CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
CC disease, infectious or autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
CC disease, asthma, allergic rhinitis, atopic dermatitis, food
CC hypersensitivity, urticaria, an immunologic disease of the lung,
CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
CC pneumonitis, a transplantation associated disease, graft rejection or
CC graft-versus-host disease. The present sequence represents a PRO protein
CC of the invention.
XX
SQ
XX Sequence 207 AA;
Query Match 100.0%; Score 1124; DB 8; Length 207;
Best Local Similarity 100.0%; Pred. No. 4.1e-109;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPFEPLASGILLMLLIPSPACCTVPPHPQTAFNCNSDLVIRAKFVGTPENVQTTLYQR 60
DB 1 MAPFEPLASGILLMLLIPSPACCTVPPHPQTAFNCNSDLVIRAKFVGTPENVQTTLYQR 60
QY 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSSEFLIAGKLDGLLHIT 120
DB 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGYFHRSHNSSEFLIAGKLDGLLHIT 120
QY 121 TCSFVAPMNSLSIAORRGFTKTYTGCECTVFPCLSIIPCKLQSGTHCLMTDQLQGSSEK 180
DB 121 TCSFVAPMNSLSIAORRGFTKTYTGCECTVFPCLSIIPCKLQSGTHCLMTDQLQGSSEK 180
QY 181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
DB 181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
RESULT 14
ADU06696
ID ADU06696 standard; protein; 207 AA.
XX
AC ADU06696;
XX
DT 27-JAN-2005 (first entry)
XX
DE Novel bronchial cancer-associated human protein SegID922.
XX
KM bronchial cancer; cytosaratic; tumour-associated protein;
KM cancer detection; metastasis; tumour; human.
XX
OS Homo sapiens.
XX
OS
XX
PN DE10316701-A1.
XX
PD 04-NOV-2004.
XX
PF 09-APR-2003; 2003DE-01016701.
XX
PR 09-APR-2003; 2003DE-01016701.
XX
```

XX (HINZ/) HINZMANN B.
 PA (HERM/) HERMANN K.
 PA (CAST/) HEIDEN CASTANOS-VELEZ E.
 XX Wennerich D, Brummeendorf T, Heiden E, Hermann K, Kinnemann H,
 PI Li X, Roeper S, Staub E, Hinzmann B, Rosenthal A, Pilarsky C;
 XX
 DR MPI: 2004-786403/78.
 DR N-PSDB; ADU06209.
 XX
 PT New nucleic acid, and derived proteins, useful for diagnosis of bronchial
 PT cancer and in screening for therapeutic and diagnostic agents.
 XX
 PS Claim 2; SEQ ID NO 922; 1381bp; German.
 XX
 CC This invention relates to a novel isolated nucleic acid associated with
 CC bronchial cancer comprising 489 defined sequences given in the
 CC specification. The invention may be useful for the production of
 CC compounds with a cytostatic activity through the inhibition of expression
 CC or activity of tumour-associated proteins. The novel DNA sequences and
 CC the proteins/peptides encoded by them are used for detecting bronchial
 CC cancer or determining the risk of developing it and to screen for
 CC specific binding partners of the DNA or protein sequences, where the
 CC binding partners are potentially useful as agents for treating or
 CC diagnosing bronchial cancer. The DNA or protein sequences can also be
 CC used for prognosis, detection of metastases and for secondary treatment
 CC (of tumours that have been stabilised or are no longer detectable).
 CC Detecting abnormal expression of the DNA sequences provides early
 CC diagnosis of bronchial cancers. The present sequence is that of a protein
 CC encoded by a novel bronchial cancer-associated human gene sequence of the
 CC invention.
 XX
 SQ Sequence 207 AA;

Query Match 100.0%; Score 1124; DB 8; Length 207;
 Best Local Similarity 100.0%; Pred. No. 4.1e-109;
 Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPEPLASGILLMLIAPSRACCTVPPHPTAFNCNSDLVIRAKFVGTEVNQTTLYOR 60
 DB 1 MAPEPLASGILLMLIAPSRACCTVPPHPTAFNCNSDLVIRAKFVGTEVNQTTLYOR 60
 QY 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGFPHSHNSEBFLAAGKLODGLHTT 120
 DB 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGFPHSHNSEBFLAAGKLODGLHTT 120
 QY 121 TCSFVAPMNSLSLAQRGFTKTYTVGCECTVFPCLSIIPCKLQSGTHCLMTDQLQSGSEK 180
 DB 121 TCSFVAPMNSLSLAQRGFTKTYTVGCECTVFPCLSIIPCKLQSGTHCLMTDQLQSGSEK 180
 QY 181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
 DB 181 GFQSRHLACLPREPGLCTWQSLRSQIA 207

RESULT 15

ADV70205
 ID ADV70205 standard; protein; 207 AA.

ADV70205;

10-MAR-2005 (first entry)

Tumour-associated antigenic target polypeptide TAT447.

Cytostatic; diagnosis; therapy; tumor;

tumor-associated antigenic target polypeptide; TAT.

Homo sapiens.

WO2004112829-A2.

XX

PD 29-DEC-2004.
 XX
 PF 21-MAY-2004; 2004WO-US016121.
 XX
 PR 23-MAY-2003; 2003US-0473238P.
 PR 27-FEB-2004; 2004US-0548299P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Philippe H;
 XX
 DR MPI; 2005-048766/05.
 DR N-PSDB; ADV70110.
 XX
 PT Treating a mammal having a tumor of glial origin comprising cells that
 PT express a type A or B glial tumor antigen by contacting the cells with a
 PT composition comprising first and second binding agents.
 XX
 PS Disclosure; SEQ ID NO 129; 374bp; English.

CC The invention describes a method of treating a mammal having a tumor of
 CC glial origin comprising cells that express a type A or B glial tumor
 CC antigen comprising contacting the cells with a composition of: a first
 CC binding agent comprising a first antibody, oligopeptide or organic
 CC molecule that binds to a type A or B glial tumor antigen; and a second
 CC binding agent comprising a second antibody, oligopeptide or organic
 CC molecule that binds to a type B or A glial tumor antigen. Also described
 CC is a method of determining the presence of a type A or B glial tumor in a
 CC mammal. The method is useful in treating a mammal having a tumor of glial
 CC origin comprising cells that express a type A or B glial tumor antigen.
 CC This sequence represents a human tumor-associated antigenic target
 CC polypeptide.
 XX
 SQ Sequence 207 AA;

Query Match 100.0%; Score 1124; DB 9; Length 207;
 Best Local Similarity 100.0%; Pred. No. 4.1e-109;
 Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPEPLASGILLMLIAPSRACCTVPPHPTAFNCNSDLVIRAKFVGTEVNQTTLYOR 60
 DB 1 MAPEPLASGILLMLIAPSRACCTVPPHPTAFNCNSDLVIRAKFVGTEVNQTTLYOR 60
 QY 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGFPHSHNSEBFLAAGKLODGLHTT 120
 DB 61 YEIKMTKMYKGFQALGDADIRFVYTPAMESVCGFPHSHNSEBFLAAGKLODGLHTT 120
 QY 121 TCSFVAPMNSLSLAQRGFTKTYTVGCECTVFPCLSIIPCKLQSGTHCLMTDQLQSGSEK 180
 DB 121 TCSFVAPMNSLSLAQRGFTKTYTVGCECTVFPCLSIIPCKLQSGTHCLMTDQLQSGSEK 180
 QY 181 GFQSRHLACLPREPGLCTWQSLRSQIA 207
 DB 181 GFQSRHLACLPREPGLCTWQSLRSQIA 207

Search completed: April 10, 2006, 18:01:20
 Job time : 84.203 secs

THIS PAGE LEFT BLANK